

58662
Delaval, Jan

From: Jamroz, Margaret
Sent: Tuesday, January 22, 2002 8:12 AM
To: Delaval, Jan
Subject: 09/628,126

Jan,

Please do open search SEQ ID NOS: 6, 8, 19, and 23 with interference for 09/628,126.

Thanks,
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USPTO
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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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	Type of Search	Vendors and cost where applicable
Searcher: <u>C. Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>12496</u>	AA Sequence (#) <u>4</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>1/22</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>1/22</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>10</u>	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:16:15 ; Search time 78.06 Seconds
(without alignments)
226.794 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MPELQAGSCGAPSPDPAM.....DTNFTPLDNLVSLYSSD 239

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 45 summaries

Database : A_Geneseq_1101.*

- 1: /SID52/gcgdata/geneseq/geneseqp/AA1980.DAT.*
- 2: /SID52/gcgdata/geneseq/geneseqp/AA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseqp/AA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseqp/AA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseqp/AA1984.DAT.*
- 6: /SID52/gcgdata/geneseq/geneseqp/AA1985.DAT.*
- 7: /SID52/gcgdata/geneseq/geneseqp/AA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneseqp/AA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneseqp/AA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneseqp/AA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneseqp/AA1990.DAT.*
- 12: /SID52/gcgdata/geneseq/geneseqp/AA1991.DAT.*
- 13: /SID52/gcgdata/geneseq/geneseqp/AA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneseqp/AA1993.DAT.*
- 15: /SID52/gcgdata/geneseq/geneseqp/AA1994.DAT.*
- 16: /SID52/gcgdata/geneseq/geneseqp/AA1995.DAT.*
- 17: /SID52/gcgdata/geneseq/geneseqp/AA1996.DAT.*
- 18: /SID52/gcgdata/geneseq/geneseqp/AA1997.DAT.*
- 19: /SID52/gcgdata/geneseq/geneseqp/AA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneseqp/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseqp/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	AA45008	Sequence encoded b
2	1141	91.6	220	AA45006	Sequence encoded b
3	860.5	69.1	234	AA45009	Sequence encoded b
4	814.5	65.4	215	AA45007	Sequence encoded b
5	742	59.6	143	AA450277	Amino acid sequenc
6	600	48.2	143	AA4508276	Amino acid sequenc
7	126	10.1	279	AA458357	Mouse Fas ligand.
8	123	9.9	279	AA459098	Mouse Fas ligand.
9	110	8.8	279	AA457282	Mouse Fas-L protei
10	109	8.7	179	AA459069	Mouse Fas ligand (
11	102	8.2	278	AA459095	Rat Fas ligand enc

12	102	8.2	278	20	AA459069	Rat Fas ligand (Fa
13	102	8.2	278	20	AA459040	Rat FasL protein.
14	97	7.8	138	16	AA459068	Mouse Fas ligand (
15	97	7.8	143	21	AA459068	Amino acid sequenc
16	96	7.7	281	22	AA459068	Human Fas ligand p
17	95.5	7.7	258	20	AA459068	Human Fas ligand d
18	95	7.6	137	16	AA459067	Mouse Fas ligand (
19	92	7.4	271	20	AA459067	Fas ligand (FasL)
20	91	7.3	179	16	AA459066	Rat Fas ligand (pa
21	91	7.3	309	16	AA459066	Murine 4-1BB-L pol
22	91	7.3	309	18	AA459066	Murine 4-1BB ligand
23	89.5	7.2	268	19	AA459066	Non-cleavable Fas
24	88.5	7.1	448	21	AA459066	PC-muAGP-1 (99-291
25	88	7.1	281	20	AA459066	Human Fas ligand d
26	88	7.1	281	21	AA459066	Human Fas ligand (
27	88	7.1	281	21	AA459066	Human Fas ligand (
28	87	7.0	265	19	AA459066	Non-cleavable Fas
29	87	7.0	277	20	AA459066	Human Fas ligand d
30	87	7.0	281	16	AA459066	Human Fas-L protei
31	87	7.0	281	16	AA459066	Human Fas ligand.
32	87	7.0	281	17	AA459066	Human Fas ligand d
33	87	7.0	281	17	AA459066	Human Fas ligand.
34	87	7.0	281	18	AA459066	Human Fas ligand.
35	87	7.0	281	18	AA459066	Human Fas ligand.
36	87	7.0	281	19	AA459066	Human Fas ligand.
37	87	7.0	281	19	AA459066	Fas ligand. Mamma
38	87	7.0	281	20	AA459066	Wild type Fas liga
39	87	7.0	281	20	AA459066	Human Fas ligand (
40	87	7.0	281	20	AA459066	Human FasL protein
41	87	7.0	281	21	AA459066	Amino acid sequenc
42	87	7.0	281	21	AA459066	Human Fas ligand (
43	87	7.0	281	21	AA459066	Human Fas ligand (
44	87	7.0	281	21	AA459066	Human Fas ligand (
45	87	7.0	281	21	AA459066	Human Fas ligand (

ALIGNMENTS

RESULT 1
AA45008
ID AA45008 standard; Protein; 239 AA.
XX
AC AA45008;
XX
DT 19-JUN-1994 (first entry)
XX
DE Sequence encoded by a murine CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX

OS Acomys cahirinus.
XX
FH key Location/Qualifiers
FT Region 47..67
FT /label= Transmembrane
XX
PN WO9324135-A.
XX
PD 09-DEC-1993.
XX
PF 25-MAY-1993; 93WO-US04926.
XX
PR 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.
PR 15-JUN-1992; 92US-0896660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
PA (IMMV) IMMUNEX CORP.
XX

PI Armitage RJ, Goodwin RG, Smith CA;
 XX WPI; 1993-405417/50.
 DR N-PSDB; AAQ53537.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 6a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
 CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
 CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
 CC anchored PCR technique was employed to isolate CD30-L human and murine
 CC clones containing an additional 19 N-terminal amino acid sequence
 CC (AAQ53537, AAQ53538).
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 1246; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.8e-116;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEFGLOAGSCGAPSPDPAMQVPGSVASPRWSTSRYSFYLSLTALVCLVAVVA 60
 Db |
 QY 61 IILVLVQKQKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSW 120
 Db |
 QY 121 NEDGTIHGLYQDGNLIVQPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180
 Db |
 QY 181 VCESGVQSKNIYQNLQFLHLYLQVNSTISVRVDNFQYVDTNTPPLDNVLSVFLYSSSD 239
 Db |
 QY 181 VCESGVQSKNIYQNLQFLHLYLQVNSTISVRVDNFQYVDTNTPPLDNVLSVFLYSSSD 239
 Db |
 RESULT 2
 AAR45006
 ID AAR45006 standard; Protein; 220 AA.
 XX
 AC AAR45006;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a murine CD30-L cDNA clone.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Acromys cahirinus.
 XX
 XX Key Location/Qualifiers
 FT Region 28..48
 FT /label= transmembrane
 XX
 PN W09324135-A.
 XX
 PD 09-DEC-1993.
 XX
 XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.
 PR 02-JUN-1992; 92US-0892459.
 PR 15-JUN-1992; 92US-0899660.
 PR 01-JUL-1992; 92US-0907224.
 PR 27-OCT-1992; 92US-0966775.
 XX (IMMV) IMMUNEX CORP.
 XX
 PI Armitage RJ, Goodwin RG, Smith CA;
 XX
 XX WPI; 1993-405417/50.
 DR N-PSDB; AAQ53535.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 3a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
 CC This cDNA can then be used as a probe to screen a human PBL cDNA
 CC library to obtain cDNA encoding human CD30-L.
 XX
 SQ Sequence 220 AA;
 Query Match 91.6%; Score 1141; DB 14; Length 220;
 Best Local Similarity 100.0%; Pred. No. 5e-106;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 MQVQPGSVASPRWSTSRYSFYLSLTALVCLVAVVAIILVLVQKQKSTPNTTEK 79
 Db |
 QY 80 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDEGTIHGLIYQDGNLIVQ 139
 Db |
 QY 61 aplkggncsedlftclktspkkskswaylqvskhlntklswnedgtihgliyqdglnliq 120
 Db |
 QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLQFL 199
 Db |
 QY 121 fpglyfivcqilqvcsnhsvdltlqlinskkikktlvtvcesgvqskniyqnlisqfl 180
 Db |
 QY 200 LHYLQVNSTISVRVDNFQYVDTNTPPLDNVLSVFLYSSSD 239
 Db |
 QY 181 lhyiqvnstisvrvdnfyvdtntfpldnvlsflysssd 220
 Db |
 RESULT 3
 AAR45009
 ID AAR45009 standard; Protein; 234 AA.
 XX
 AC AAR45009;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a human CD30-L cDNA clone
 DE encoding additional N-terminal amino acids.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 41..62

FT XX /label= Transmembrane

PN WO9324135-A.

XX 09-DEC-1993.

PD 25-MAY-1993;

XX 93WO-US04926.

XX 26-MAY-1992;

XX 92US-0889717.

XX 02-JUN-1992;

XX 92US-0892459.

XX 15-JUN-1992;

XX 92US-0899660.

XX 01-JUL-1992;

XX 92US-0907224.

XX 27-OCT-1992;

XX 92US-0966775.

XX (IMMV) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

XX N-PSDB; AAQ53538.

XX New cytokine, CD30-L, which binds CD30 - used for developing

XX prods. for diagnosis, detection, purifications, research and

XX therapy

XX Claim 15; Figure 7a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

XX as a clinical marker for Hodgkin's lymphoma and related haematologic

XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

XX L and other derived prods. can be used for elucidating the roles

XX that CD30 and CD30-L may play in the immune system and for diagnosis

XX and therapy. It can be isolated as follows. A cDNA library prepd. from

XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion

XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L

XX (AAQ53535). This cDNA can then be used as a probe to screen a human PBL

XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An

XX anchored PCR technique was employed to isolate CD30-L human and murine

XX clones containing an additional 19 N-terminal amino acid sequence

XX (AAQ53537, AAQ53538).

XX Sequence 234 AA;

XX Query Match 69.1%; Score 860.5; DB 14; Length 234;

XX Best Local Similarity 69.6%; Pred. No. 5.9e-78;

XX Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

XX 1 MEPGLQAGCGAPSDPDAMQVPGSVASPMRSTRPWRSTRSYFYLTSTAL-VCLVVAV 59

XX 1 mdpqlqalngmappgdgtamhpagvas-----hlgttsrlyfytatlalclvftv 54

XX 60 AITLVLVVOKKSTPTNTEKAPLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLS 119

XX 55 atlmvlvrtidsipnsdpnvlpgkncsedllclkrpfkkswaylqvahlnktkls 114

XX 120 WNEDGTIHLGLIVQDGLNLIYFVCOLOFVQCSNHSVDLTQLLINSKIKKOTLV 179

XX 115 wnkdgilhvryqdgnlvqfplyfiicqlqlvqcpnmsvdkellinkhikkalv 174

XX 180 TVCEGVSQKNTIYQNIQSQFLLHYLQVNSTISVRVDFNQYVDTNTPFDNLVSLYSSD 239

XX 175 tvcesgmqtkhvyqnlsgfildylqvnttissvndtftqyidstfplenvlsiflynsd 234

XX RESULT 4

XX AAR45007

XX ID AAR45007 standard; Protein; 215 AA.

XX AC AAR45007;

XX 19-JUN-1994 (first entry)

XX DT

XX XX

DE

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XX

Sequence encoded by a human CD30-L cDNA clone.

Hodgkin's disease; lymphoma; surface antigen; cytokine;

CD30 ligand; CD30-L; TNF; NGF.

Homo sapiens.

Key

Location/Qualifiers

Region

/label= transmembrane

WO9324135-A.

09-DEC-1993.

25-MAY-1993;

93WO-US04926.

26-MAY-1992;

92US-0889717.

02-JUN-1992;

92US-0892459.

15-JUN-1992;

92US-0899660.

01-JUL-1992;

92US-0907224.

27-OCT-1992;

92US-0966775.

(IMMV) IMMUNEX CORP.

Armitage RJ, Goodwin RG, Smith CA;

WPI; 1993-405417/50.

N-PSDB; AAQ53536.

New cytokine, CD30-L, which binds CD30 - used for developing

prods. for diagnosis, detection, purifications, research and

therapy

Claim 15; Figure 5a; 59pp; English.

CD30-L is a ligand for CD30, the 120kd surface antigen widely used

as a clinical marker for Hodgkin's lymphoma and related haematologic

malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

L and other derived prods. can be used for elucidating the roles

that CD30 and CD30-L may play in the immune system and for diagnosis

and therapy. It can be isolated as follows. A cDNA library prepd. from

the murine helper T-cell line 7B9 is screened with a CD30/FC fusion

protein labelled with (125)I to obtain cDNA encoding murine CD30-L.

This cDNA can then be used as a probe to screen a human PBL cDNA

library to obtain cDNA encoding human CD30-L.

Sequence 215 AA;

Query Match 65.4%; Score 814.5; DB 14; Length 215;

Best Local Similarity 70.6%; Pred. No. 2.1e-73;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

20 MQVPGSVASPMRSTRPWRSTRSYFYLTSTAL-VCLVVAVAILLVVQKSDSTPTNTE 78

1 mhpvagsvas-----hlgttsrlyfytatlalclvftvatimlvvqtdsipsnd 54

79 KAPLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLGLIVQDGLNLI 138

55 nvplkkgncsedllclkrpfkkswaylqvahlnktklswnkdgilhvryqdgnlvi 114

139 QPGLYFTVCOLOFVQCSNHSVDLTQLLINSKIKKOTLVTVCEGVSQKNTIYQNLISOF 198

115 qfpglyfiicqlqlvqcpnmsvdkellinkhikkalvltvcesgmqtkhvyqnlsgf 174

199 LLHYLQVNSTISVRVDFNQYVDTNTPFDNLVSLYSSD 239

175 lllylqvnttissvndtftqyidstfplenvlsiflynsd 215

RESULT 5

AAB08277

QY 54 CLVVAVAILIIVVOKKSTPNTTEKAPLKGGNCSEDLFCTLKSTPSKK-----SWAYLOV 109
 Db 94 gm--g1gmyqifh1qkelaelfnqslkvsfekql--anpstpskkprsvahltg 149
 QY 110 SKHLNNTKLSWNEB-GT--IHGLIYQDGNLIVQPPGLYFIVCOLQFLVQ-CSNHSVDLT 165
 Db 150 nphsrsip1ewedygtal1sgvkykkg1vinetg1lyfyyskvyf1gqscnnqplnhkv 209
 QY 166 QLLINSK-----IKKOTLVTVCESG-----VQSKNIYQNLISQFLHLYLQ 204
 Db 210 ymr-nskyped1vmeekrlnycttg1wahssylgavfnltsadhl1yvn1sq1sl1nfe 268
 QY 205 VNST 208
 Db 269 eskt 272

RESULT 9
 AAR77282
 ID AAR77282 standard; Protein; 279 AA.
 XX
 AC AAR77282;
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE Mouse Fas-L protein.
 XX
 KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
 KW self-tolerance.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..78
 FT Domain /label= Cytoplasmic_domain
 FT Domain 79..103
 FT Domain /label= Transmembrane_domain
 FT Domain 104..279
 FT Domain /label= Extracellular_domain
 XX
 PN W09518819-A.
 XX
 PD 13-JUL-1995.
 XX
 PF 06-JAN-1995; 95WO-US00362.
 XX
 PR 01-FEB-1994; 94US-0190559.
 PR 07-JAN-1994; 94US-0179138.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Goodwin RG;
 XX
 DR WPI; 1995-255032/33.
 DR N-PSDB; AAQ91312.
 XX
 PT Human and murine DNA encoding ligand(s) binding to cell surface protein
 PT Fas - useful for studying auto-immune disorder(s) and development of
 PT self-tolerance.
 XX
 PS Disclosure; Page 29-30; 38pp; English.
 XX
 CC A cDNA library prep'd. from mouse peripheral blood lymphocyte mRNA was
 CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
 CC An isolated clone (AAQ91312) encoded mouse Fas-L.
 XX
 SQ Sequence 279 AA;

Query Match 8.8%; Score 110; DB 16; Length 279;
 Best Local Similarity 21.9%; Pred. No. 0.0077;
 Matches 55; Conservative 42; Mismatches 104; Indels 50; Gaps 11;

QY 10 SCG-----APSPDPAMQVQPSVASPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 60
 Db 34 scgprgdqrrppppppvpsipppsqplsp1pltkkdh-----tnlwlpvv 84
 QY 61 IILVL-----VVOKKSTPNTTEKAPLKGGNCSEDLFCTLKSTPSKK----- 102
 Db 85 fmv1qkelaelfnqslkelaelfnqslkvsfekql--anpstpskkpr 142
 QY 103 SWAYLOVSKHLNNTKLSWNEB-GT--IHGLIYQDGNLIVQPPGLYFIVCOLQFLVQ-CSN 158
 Db 143 svahltgphsrsip1ewedygtal1sgvkykkg1vinetg1lyfyyskvyf1gqscnn 202
 QY 159 HSDVLTQLLLINSKTKOTLVTVCESGVQSKNI-YQNLISQFLHLYLQVNSTISVRVDNFQ 217
 Db 203 qplnhkvymr-nskyped1v-----meekrlnyfttg1wahssylgavfnltsadhl 255
 QY 218 VVDNTNTPFLDN 228
 Db 256 yvn1sq1sl1n 266

RESULT 10
 AAR79069
 ID AAR79069 standard; Protein; 179 AA.
 XX
 AC AAR79069;
 XX
 DT 22-FEB-1996 (first entry)
 XX
 DE Mouse Fas ligand (partial sequence).
 XX
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
 KW Fas cell surface antigen; Fas-L; mouse.
 XX
 OS Mus musculus.
 XX
 PN W09513293-A1.
 XX
 PD 18-MAY-1995.
 XX
 PF 10-NOV-1994; 94WO-JP01899.
 XX
 PR 18-OCT-1994; 94JP-0278378.
 PR 10-NOV-1993; 93JP-0305975.
 PR 13-DEC-1993; 93JP-0342526.
 PR 18-MAR-1994; 94JP-0074344.
 PR 08-JUL-1994; 94JP-0180955.
 PR 07-SEP-1994; 94JP-0239363.
 XX
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAXA BIOSCIENCE INST.
 XX
 PI Nagata S, Nakamura N, Suda T, Takahashi T;
 XX
 DR WPI; 1995-194031/25.
 DR N-PSDB; AAQ99498.
 XX
 PT Peptide which binds to Fas antigen, and antibody reactive with it
 PT for treatment and diagnosis of viral or auto-immune diseases
 XX
 PS Claim 11; Page 222-224; 300pp; Japanese.
 XX
 CC Fas ligands or active fragments able to induce apoptosis in cells
 CC which express the Fas cell surface antigen are claimed. The
 CC proteins are isolated from human, rat and mouse sources. The present
 CC sequence represents part of the mouse Fas ligand.
 XX
 SQ Sequence 179 AA;

Query Match 8.7%; Score 109; DB 16; Length 179;
 Best Local Similarity 26.2%; Pred. No. 0.0053;
 Matches 37; Conservative 28; Mismatches 46; Indels 30; Gaps 7;

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	1141	100.0	220	14 AAR45006	Sequence encoded b
2	1141	100.0	239	14 AAR45008	Sequence encoded b
3	814.5	71.4	215	14 AAR45007	Sequence encoded b
4	814.5	71.4	234	14 AAR45009	Sequence encoded b
5	742	65.0	143	21 AAB08277	Amino acid sequenc
6	600	52.6	143	21 AAB08276	Amino acid sequenc
7	112	9.8	279	16 AAR88357	Mouse Fas ligand.
8	109	9.6	179	16 AAR79069	Mouse Fas ligand.
9	109	9.6	279	16 AAR79098	Mouse Fas ligand.
10	104	9.1	279	16 AAR77282	Mouse Fas-L protei
11	97	8.5	138	16 AAR79068	Mouse Fas ligand

```

XX DR WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53535.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 3a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cDNA library prepd. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX CC This cDNA can then be used as a probe to screen a human PBL cDNA
XX CC library to obtain cDNA encoding human CD30-L.
XX SQ Sequence 220 AA;
Query Match 100.0%; Score 1141; DB 14; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.8e-108;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOVQPGSVASPRWSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
DB 1 mqvpgsvasprwstsrysfyltalvclvavaillvvqkkdstpnttek 60
QY 61 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
DB 61 aplkggncsedlftclkstpskswaylqvskhlnntklswnedgtihgliyqdggnliqv 120
QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCEGVSQSKNIYQNLQSFL 180
DB 121 fpglyfivcqlqflvqcshsvdltqlllnnskikktlvtvcesgvsqskniyqnlqsfl 180
QY 181 LHYLVQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 220
DB 181 lhylvqvnstisvrvdnfyvdtntfpdlnvlsflysssd 220
RESULT 2
AAR45008
ID AAR45008 standard; Protein; 239 AA.
XX AC AAR45008;
XX DT 19-JUN-1994 (first entry)
XX DE Sequence encoded by a murine CD30-L cDNA clone
XX DE encoding additional N-terminal amino acids.
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
XX KW CD30 ligand; CD30-L; TNF; NGF.
XX OS Acomys cahirinus.
XX XX
XX FH Key Location/Qualifiers
XX FT Region 47..67
XX FT /label= Transmembrane
XX XX
XX PN W09324135-A.
XX XX
XX PD 09-DEC-1993.
XX XX
XX PF 25-MAY-1993; 93WO-US04926.
XX XX
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.

```

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PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX PA (IMNV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX XX
XX DR WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53537.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 6a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cDNA library prepd. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX CC anchored PCR technique was employed to isolate CD30-L human and murine
XX CC clones containing an additional 19 N-terminal amino acid sequence
XX CC (AAQ53537, AAQ53538).
XX SQ Sequence 239 AA;
Query Match 100.0%; Score 1141; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.1e-108;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOVQPGSVASPRWSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
DB 20 mqvpgsvasprwstsrysfyltalvclvavaillvvqkkdstpnttek 79
QY 61 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
DB 80 aplkggncsedlftclkstpskswaylqvskhlnntklswnedgtihgliyqdggnliqv 139
QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCEGVSQSKNIYQNLQSFL 180
DB 140 fpglyfivcqlqflvqcshsvdltqlllnnskikktlvtvcesgvsqskniyqnlqsfl 199
QY 181 LHYLVQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 220
DB 200 lhylvqvnstisvrvdnfyvdtntfpdlnvlsflysssd 239
RESULT 3
AAR45007
ID AAR45007 standard; Protein; 215 AA.
XX AC AAR45007;
XX DT 19-JUN-1994 (first entry)
XX DE Sequence encoded by a human CD30-L cDNA clone.
XX DE Hodgkin's disease; lymphoma; surface antigen; cytokine;
XX KW CD30 ligand; CD30-L; TNF; NGF.
XX KW
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Region 22..43
XX FT /label= transmembrane

```

XX WO9324135-A.
 XX 09-DEC-1993.
 XX 25-MAY-1993; 93WO-US04926.
 XX 26-MAY-1992; 92US-0889717.
 XX 02-JUN-1992; 92US-0892459.
 XX 15-JUN-1992; 92US-0899660.
 XX 01-JUL-1992; 92US-0907224.
 XX 27-OCT-1992; 92US-0966775.
 XX (IMMV) IMMUNEX CORP.

PI Armitage RJ, Goodwin RG, Smith CA;

DR WPI; 1993-405417/50.

DR N-PSDB; AAQ53536.

PT New cytokine, CD30-L, which binds CD30 - used for developing prods. for diagnosis, detection, purifications, research and therapy

PS Claim 15; Figure 5a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used as a clinical marker for Hodgkin's lymphoma and related haematologic malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-L and other derived prods. can be used for elucidating the roles that CD30 and CD30-L may play in the immune system and for diagnosis and therapy. It can be isolated as follows. A cDNA library prep. from the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion protein labelled with (125)I to obtain cDNA encoding murine CD30-L. This cDNA can then be used as a probe to screen a human PBL cDNA library to obtain cDNA encoding human CD30-L.

XX Sequence 215 AA;

Query Match 71.4%; Score 814.5; DB 14; Length 215;

Best Local Similarity 70.6%; Pred. No. 5e-75;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MOVQPGSVASPWRSRTPWRSTSRSYFYLTSTAL-VCLVAVAVAILVLVWVKDSTPNTTE 59

DB 1 mhvpagsvas-----hlgtsrsyfytatlaclvftvatimlvvgtdsipsnd 54

QY 60 KAPLKGNCSEDLFCFLTKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119

55 nvpikgncsedllcilkrapfkkswaylqvakhlnktlswnkdgilhgvyqdglnlvi 114

QY 120 QFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLISQF 179

DB 115 qfpglyfiicqlqflvqcpnnsvdlllellinkhkkqalvtvcsgmgtkhvyqnlisqf 174

QY 180 LLHYLQVNSTISVRVDFVDTNFTPLDNVLSVFLYSSSD 220

DB 175 lldylqvnttissvndtftfyidstfplenvlsiflynsnd 215

RESULT 4

AAR45009

ID AAR45009 standard; Protein; 234 AA.

XX AC AAR45009;

XX 19-JUN-1994 (first entry)

XX Sequence encoded by a human CD30-L cDNA clone

DE encoding additional N-terminal amino acids.

XX

XX Hodgkin's disease; lymphoma; surface antigen; cytokine;

KW CD30 ligand; CD30-L; TNF; NGF.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 41..62
 FT /label= Transmembrane

XX WO9324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

XX 02-JUN-1992; 92US-0892459.

XX 15-JUN-1992; 92US-0899660.

XX 01-JUL-1992; 92US-0907224.

XX 27-OCT-1992; 92US-0966775.

XX (IMMV) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

XX N-PSDB; AAQ53538.

XX New cytokine, CD30-L, which binds CD30 - used for developing prods. for diagnosis, detection, purifications, research and therapy

XX Claim 15; Figure 7a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used as a clinical marker for Hodgkin's lymphoma and related haematologic malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-L and other derived prods. can be used for elucidating the roles that CD30 and CD30-L may play in the immune system and for diagnosis and therapy. It can be isolated as follows. A cDNA library prep. from the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion protein labelled with (125)I to obtain cDNA encoding murine CD30-L. This cDNA can then be used as a probe to screen a human PBL cDNA library to obtain cDNA encoding human CD30-L.

XX Sequence 234 AA;

Query Match 71.4%; Score 814.5; DB 14; Length 234;

Best Local Similarity 70.6%; Pred. No. 5.6e-75;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MOVQPGSVASPWRSRTPWRSTSRSYFYLTSTAL-VCLVAVAVAILVLVWVKDSTPNTTE 59

DB 20 mhvpagsvas-----hlgtsrsyfytatlaclvftvatimlvvgtdsipsnd 73

QY 60 KAPLKGNCSEDLFCFLTKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119

DB 74 nvpikgncsedllcilkrapfkkswaylqvakhlnktlswnkdgilhgvyqdglnlvi 133

QY 120 QFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLISQF 179

DB 134 qfpglyfiicqlqflvqcpnnsvdlllellinkhkkqalvtvcsgmgtkhvyqnlisqf 193

QY 180 LLHYLQVNSTISVRVDFVDTNFTPLDNVLSVFLYSSSD 220

DB 194 lldylqvnttissvndtftfyidstfplenvlsiflynsnd 234

RESULT 5

AAB08277

ID AAB08277 standard; Protein; 143 AA.

AC AAB08277;

XX 04-DEC-2000 (first entry)

DE Amino acid sequence of a mouse TNF ligand CD30L.

XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.

XX Mus sp.

PN WO200047740-A2.

XX 17-AUG-2000.

PF 11-FEB-2000; 2000WO-US03653.

XX 12-FEB-1999; 99US-0119906.

PR 18-NOV-1999; 99US-0166271.

XX (AMGE-) AMGEN INC.

PI Boyle WJ, Hsu H;

XX WPI; 2000-558217/51.

XX Novel polypeptides comprising tumour necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis -

PS Claim 14; Fig 9; 7lpp; English.

XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand
CC family member. AGP-3 is a type II transmembrane protein, and is a
CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
CC increases in the number of B cells and immunoglobulins produced.
CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
CC Crohn's disease, lupus and graft versus host disease. The nucleic
CC acids may be used to regulate the expression of an AGP-3 related
CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
CC useful for the detection of AGP-3 agonists, antagonists and
CC characterizing interactions with AGP-3 related proteins.

XX Sequence 143 AA;

Query Match 65.0%; Score 742; DB 21; Length 143;

Best Local Similarity 100.0%; Pred. No. 7e-68;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 STPSKSWAYLOYSKHLNNTKLSWNEDGTHGLIYQDGNLIVQPGLYFIVCQLQFLVQC 137

Db 1 stpskswaylvqskhlntklswnedgthgllyqdglnlvqpglyfivcqlqflvqc 60

Qy 138 SNHSDVLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLQSFLLHYLQVNSTISVRVDF 197

Db 61 snhsdvltqlllnskkkqtlvtvcesgvqskniyqnlqsfllhyqlvnstisvrdf 120

Qy 198 QYVDTNFTPLDNVLSVFLYSSSD 220

Db 121 qyvdtntfpldnvlsflysssd 143

RESULT 6

AAB08276

ID AAB08276 standard; Protein; 143 AA.

XX

AC AAB08276;

XX 04-DEC-2000 (first entry)

DE Amino acid sequence of a human TNF ligand CD30L.

XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.

XX Homo sapiens.

PN WO200047740-A2.

XX 17-AUG-2000.

PF 11-FEB-2000; 2000WO-US03653.

XX 12-FEB-1999; 99US-0119906.

PR 18-NOV-1999; 99US-0166271.

XX (AMGE-) AMGEN INC.

PI Boyle WJ, Hsu H;

XX WPI; 2000-558217/51.

XX Novel polypeptides comprising tumour necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis -

PS Claim 14; Fig 9; 7lpp; English.

XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand
CC family member. AGP-3 is a type II transmembrane protein, and is a
CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
CC increases in the number of B cells and immunoglobulins produced.
CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
CC Crohn's disease, lupus and graft versus host disease. The nucleic
CC acids may be used to regulate the expression of an AGP-3 related
CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
CC useful for the detection of AGP-3 agonists, antagonists and
CC characterizing interactions with AGP-3 related proteins.

XX Sequence 143 AA;

Query Match 52.6%; Score 600; DB 21; Length 143;

Best Local Similarity 77.3%; Pred. No. 2.1e-53;

Matches 109; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

Qy 80 PSKSWAYLOYSKHLNNTKLSWNEDGTHGLIYQDGNLIVQPGLYFIVCQLQFLVQC 139

Db 3 pfkkswaylvqskhlntklswnedgthgllyqdglnlvqpglyfivcqlqflvqc 62

Qy 140 HSDVLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLQSFLLHYLQVNSTISVRVDF 199

Db 63 nsdvltqlllnskkkqtlvtvcesgvqskniyqnlqsfllhyqlvnstisvrdf 122

Qy 200 VDTNFTPLDNVLSVFLYSSSD 220

Db 123 idtstfpldnvlsflysssd 143

RESULT 7

AAR8357

ID AAR8357 standard; Protein; 279 AA.

XX

AC AAR8357;

XX


```

PF 10-NOV-1994; 94WO-JF01899.
XX
PR 18-OCT-1994; 94JP-0278378.
PR 10-NOV-1993; 93JP-0305975.
PR 13-DEC-1993; 93JP-0342526.
PR 18-MAR-1994; 94JP-0074344.
PR 08-JUL-1994; 94JP-0180955.
PR 07-SEP-1994; 94JP-0239363.
XX
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S., Nakamura N, Suda T, Takahashi T;
XX WPI; 1995-194031/25.
DR N-PSDB; AAQ99496.
XX
XX Peptide which binds to Fas antigen, and antibody reactive with it
XX for treatment and diagnosis of viral or auto-immune diseases
XX
XX Claim 9; Page 219-221; 300pp; Japanese.
XX
XX Fas ligands or active fragments able to induce apoptosis in cells
XX which express the Fas cell surface antigen are claimed. The
XX proteins are isolated from human, rat and mouse sources. The present
XX sequence represents part of the mouse Fas ligand.
XX
XX Sequence 137 AA;
SQ
Query Match 8.3%; Score 95; DB 16; Length 137;
Best Local Similarity 24.4%; Pred. No. 0.057;
Matches 32; Conservative 27; Mismatches 46; Indels 26; Gaps 6;
OY 84 SWAYLQVSKHLNNTKLSWNED-GT--IHGLIYQDGNLIVQPPGLYFIVCQLOFLVQ-CSN 139
Db 1 svahltnghrsrslpewedytgallsgvxykkggvinetgylfvyvsgqscnn 60
OY 140 HSYDLTLQLLNSK-----IKQTLLTVTCESG-----VQSKNIYQNLQSQ 178
Db 61 qpinkhkvymr-nskypedlvmeeekrlnyctgtgiahssylgavfalsadhylnvnisq 119
OY 179 FLHYLYQVNST 189
Db 120 lslinfeeskt 130
RESULT 14
AAU04556
ID AAU04556 standard; Protein; 281 AA.
XX
XX AAU04556;
XX
XX 26-SEP-2001 (first entry)
XX
XX Human Fas ligand protein, FasL.
XX
XX Human; FasL; tumour necrosis factor; apoptosis; cancer; tumour;
XX hepatocellular carcinoma.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 120 /note= "Encoded by CAG"
XX Misc-difference 227 /note= "Encoded by GGC"
XX Misc-difference 265 /note= "Encoded by CCT"
XX
XX Wo200151503-A1.
XX
XX 19-JUL-2001.
XX

```

```

XX 04-JAN-2001; 2001WO-US00529.
PF
XX
XX 07-JAN-2000; 2000US-0479524.
PR
XX
XX (BIOC-) BIOCRYSTAL LTD.
PA
XX
XX Barbera-Guillem E;
PI
XX
XX WPI; 2001-442131/47.
DR N-PSDB; AAS08454.
XX
XX New polynucleotides comprising Fas ligand sense, Fas ligand antisense
XX polynucleotides or their combinations, for inhibiting solid nonlymphoid
XX tumour progression in an individual.
XX
XX Example 1; Page 37-39; 43pp; English.
XX
XX The sequence is the Human Fas ligand, FasL, a type II transmembrane
XX protein of the tumour necrosis factor family. Fas mediated apoptosis
XX requires cross-linking with FasL. FasL polynucleotides, antisense FasL
XX polynucleotides and their combinations are used in the manufacture of a
XX pharmaceutical composition for inhibiting tumour progression in an
XX individual, by administering the composition intratumorally into the
XX solid tumour of the individual. Types of tumours and cancers
XX include hepatocellular carcinoma and non-lymphoid tumours of the brain,
XX liver, lung, lymph node, bone marrow, breast, colon, pancreas, stomach,
XX prostate, or reproductive tract.
XX
XX Sequence 281 AA;
SQ
Query Match 8.2%; Score 93; DB 22; Length 281;
Best Local Similarity 21.3%; Pred. No. 0.24;
Matches 44; Conservative 37; Mismatches 62; Indels 64; Gaps 10;
OY 34 VCLVVAVAIILVLV-----QKKDSTPN--TTEKAPLKGNGCSEDLFC 74
Db 81 lc1lvmfvmvalvglgmfglqhlqkelaelrestsnmtasslekgihps----- 135
OY 75 TLKSTPSKKS---AYLQVSKHLNNTKLSWNEDGHI---HGLIYQDGNLIVQPPGLYFIV 128
Db 136 ---pppekkelrkvhaltgksnsrsmplewedygillsgvxykkggvinetgylfvy 192
OY 129 COLOFLVQ-CSN---HSVDLTLQLLNSK-----IKQTLLTVTCESG----- 166
Db 193 skvyfrgscnnlplshkv-----ymrnskyppqdlvmmeeknmnsycttgmmwarsylga 247
OY 167 ----VQSKNIYQNLQSQFLHYLYQVNST 189
Db 248 vfnltsadhylnvsvslsvnfeesqt 274
RESULT 15
AAU04371
ID AAU04371 standard; Protein; 258 AA.
XX
XX AAU04371;
XX
XX 24-JUN-1999 (first entry)
XX
XX Human Fas ligand derivative #1.
XX
XX Human; Fas ligand derivative; antagonist; apoptosis modulator;
XX apoptosis inducer; cytotoxic activity; protease resistant; cancer;
XX viral infection; autoimmune disease; gene therapy.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO9914325-A1.
XX
XX 25-MAR-1999.
XX

```

```
XX 17-SEP-1998; 98WO-JP04187.
PF
XX 17-SEP-1997; 97JP-0252541.
PR
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
PI Nagata S, Tanaka M;
XX
XX WPI; 1999-229531/19.
DR N-PSDB; AAX33116.
XX
PT Protease-resistant Fas ligand derivatives used for prevention of,
PT e.g. cancer
XX
PS Claim 4; Page 46-47; 60pp; Japanese.
XX
CC The present sequence is a protease-resistant Fas ligand derivative
CC in which a region of human Fas ligand which is susceptible to protease
CC attack has been deleted. The present invention also describes apoptosis
CC modulators containing soluble Fas ligand. The modification in the Fas
CC ligand renders it resistant to the action of proteases such as the
CC metalloproteinase which in vivo cleaves the active membrane-bound Fas
CC ligand (which is active as an apoptosis inducer). The Fas ligand can be
CC used for the prevention and treatment of diseases such as cancer, viral
CC infection and autoimmune disease, e.g. by introduction of DNA encoding
CC the modified Fas ligand into effector cells using a suitable gene
CC therapy vector.
XX
SQ Sequence 258 AA;

Query Match      8.1%; Score 92.5; DB 20; Length 258;
Best Local Similarity 21.0%; Pred. No. 0.24;
Matches 42; Conservative 32; Mismatches 53; Indels 73; Gaps 9;

QY 34 VCLVAVAILVLV-----QKSDTPNTERKAPLKGNCSEDLFCTLKSTPS 81
   :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|
Db 81 lcilvmfmvlgvalvglgmfglhlqkepspp-----pe 116

QY 82 KKS-----AYLQVSKHLNNTKLSWNEDGTI---HGLIYQGNLIVQPGLYFIVCQLQFLV 135
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 117 kkelrkvahltgksnrsrnpIewedygIvllsgvkYkkgIvlnetglyfyvyskvyfgr 176

QY 136 Q-CSN---HSVDLTLLQLLNSK-----IKKQTLVTVCESG-----VQS 169
   | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 qscnplplshkv-----ymrnskyppqdlvmegkmmsycttgqmwarsylgavfntsa 231

170 KNIYQNLSQLLHYLQVNST 189
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
232 dhlyvnselsivnfeesqt 251
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Search completed: January 22, 2002, 08:21:18
Job time: 303 sec

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:21:17 ; Search time 78.06 Seconds
(without alignments)
222.049 Million cell updates/sec

Title: US-09-628-126-8
Perfect score: 1220
Sequence: 1 MDPGLQALNGMAPPDGTAM.....DTSTFPLENVLISFLYSNSD 234

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1220	100.0	234	14 AAR45009	Sequence encoded b
2	1118	91.6	215	14 AAR45007	Sequence encoded b
3	860.5	70.5	239	14 AAR45008	Sequence encoded b
4	814.5	66.8	220	14 AAR45006	Sequence encoded b
5	741	60.7	143	21 AAB08276	Amino acid sequenc
6	608	49.8	143	21 AAB08277	Amino acid sequenc
7	115	9.4	279	17 AAR83357	Mouse Fas ligand.
8	112	9.2	179	16 AAR79069	Mouse Fas ligand (
9	112	9.2	279	16 AAR79098	Mouse Fas ligand.
10	108	8.9	143	21 AAB08266	Amino acid sequenc
11	106	8.7	138	16 AAR79068	Mouse Fas ligand (

12	104	8.5	137	16	AAR79067	Mouse Fas ligand (
13	102	8.4	279	16	AAR77282	Mouse Fas-L protei
14	97	8.0	268	19	AAW48953	Non-cleavable Fas
15	96.5	7.9	265	19	AAW48954	Non-cleavable Fas
16	95	7.8	180	18	AAW10875	FasL/IT-alpha hybr
17	94.5	7.7	281	22	AAU04556	Human Fas ligand p
18	93	7.6	216	19	AAW68412	Hybrid alpha-1-thy
19	92	7.5	378	18	AAW35864	Human FAS-ligand:I
20	91.5	7.5	252	22	AAW66308	FasL fusion constr
21	91.5	7.5	261	20	AAW28597	Fas ligand (FasL)
22	91.5	7.5	281	21	AAW87581	Human Fas ligand (
23	91.5	7.5	376	21	AAW52588	Secreted modified
24	91	7.5	159	22	AAW66305	FasL fusion constr
25	91	7.5	258	20	AAW04371	Human Fas ligand d
26	90.5	7.4	145	18	AAW35848	Human FAS-ligand f
27	90.5	7.4	151	18	AAW16667	Human Fas ligand (
28	90.5	7.4	178	16	AAW88308	C-terminally delet
29	90.5	7.4	179	16	AAW79099	Human Fas ligand (
30	90.5	7.4	179	18	AAW11814	Fas ligand. Homo
31	90.5	7.4	213	22	AAW66306	FasL fusion constr
32	90.5	7.4	213	22	AAW66307	FasL fusion constr
33	90.5	7.4	271	20	AAW28596	Fas ligand (FasL)
34	90.5	7.4	277	20	AAW28595	Fas ligand (FasL)
35	90.5	7.4	277	20	AAW04372	Human Fas ligand d
36	90.5	7.4	281	16	AAW77281	Human Fas-L protei
37	90.5	7.4	281	16	AAW79097	Human Fas ligand.
38	90.5	7.4	281	17	AAW98104	Human Fas ligand d
39	90.5	7.4	281	17	AAW88356	Human Fas ligand.
40	90.5	7.4	281	18	AAW27143	Human Fas ligand.
41	90.5	7.4	281	19	AAW75959	Human Fas ligand.
42	90.5	7.4	281	19	AAW49105	Fas Ligand. Mamma
43	90.5	7.4	281	20	AAW28594	Wild type Fas liga
44	90.5	7.4	281	20	AAW04373	Human Fas ligand d
45	90.5	7.4	281	20	AAW98071	Human Fas ligand (

ALIGNMENTS

RESULT 1
AAR45009
ID AAR45009 standard; Protein; 234 AA.
XX
XX AAR45009;
XX
XX
DT 19-JUN-1994 (first entry)
XX
DE Sequence encoded by a human CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 41..62
FT /label= Transmembrane
XX
XX WO9324135-A.
XX
XX 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.
PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV) IMMUNEX CORP.

PI Armitage RJ, Goodwin RG, Smith CA;
 XX WPI: 1993-405417/50.
 DR N-PSDB; AAQ53538.
 XX
 DR New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 7a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
 CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
 CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
 CC anchored PCR technique was employed to isolate CD30-L human and murine
 CC clones containing an additional 19 N-terminal amino acid sequence
 CC (AAQ53537, AAQ53538).
 XX
 SQ Sequence 234 AA;
 Query Match 100.0%; Score 1220; DB 14; Length 234;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-124;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPGLQALNGMAPPGDTAMHPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVL 60
 DB 1 mdpplgqalngmappgdtamhpagsvashlgttsrlyfytatlaiclvftvatimvl 60
 QY 61 VVQRTSDIPNSPDNPVLKGGNCSDELICILKRAPFKKSWAYLQVAKHLNKTLSWNRDGI 120
 DB 61 vvtqtdsipsndpnlkgnscsedilicilkrappfkkswaylvakhlntklswnrkdg 120
 QY 121 LHGVRYQDGNLVTFQFGLYFIICQLQFLVOCPPNNSVDLKLLELLINKHKKQALVTVCESG 180
 DB 121 lhgvrlyqdgnlvtfqfplyfiicqlqflvqcpnnsvdlkelllnkhkkqalvtvcesg 180
 QY 181 MQTKHYVQNLQFLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234
 DB 181 mqtckhyvqnlsqflldylvqnttissvndtfqyidstfplenvlsiflysnsd 234
 RESULT 2
 AAR45007
 ID AAR45007 standard; Protein; 215 AA.
 XX
 XX AAR45007;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a human CD30-L cDNA clone.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 22..43
 FT /label= transmembrane
 XX
 XX W09324135-A.
 PN
 XX
 PD 09-DEC-1993.
 XX
 XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.
 PR 02-JUN-1992; 92US-0892459.
 PR 15-JUN-1992; 92US-0895660.
 PR 01-JUL-1992; 92US-0907224.
 PR 27-OCT-1992; 92US-0966775.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Armitage RJ, Goodwin RG, Smith CA;
 XX
 DR WPI: 1993-405417/50.
 DR N-PSDB; AAQ53536.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 5a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
 CC This cDNA can then be used as a probe to screen a human PBL cDNA
 CC library to obtain cDNA encoding human CD30-L.
 XX
 SQ Sequence 215 AA;
 Query Match 91.6%; Score 1118; DB 14; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4, 2e-113;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTSDIPNSPDNPVLK 79
 DB 1 mhvpagsvashlgttsrlyfytatlaiclvftvatimlvvqtdsipsndpnlkg 60
 QY 80 GNCSDELICILKRAPFKKSWAYLQVAKHLNKTLSWNRDGIHGVRYQDGNLVTFQFGLY 139
 DB 61 gncsedilicilkrappfkkswaylvakhlntklswnrkdgilhgvrlyqdgnlvtfq 120
 QY 140 FIICQLQFLVOCPPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYVQNLQFLDY 199
 DB 121 fiicqlqflvqcpnnsvdlkelllnkhkkqalvtvcesgmqtckhyvqnlsqflldyl 180
 QY 200 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234
 DB 181 vnttissvndtfqyidstfplenvlsiflysnsd 215
 RESULT 3
 AAR45008
 ID AAR45008 standard; Protein; 239 AA.
 XX
 XX AAR45008;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a murine CD30-L cDNA clone
 DE encoding additional N-terminal amino acids.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Acomys cahirinus.
 XX
 XX Key Location/Qualifiers
 FT Region 47..67

ID AAB08276 standard; Protein; 143 AA.
XX AAB08276;
AC
XX
DT
XX
DE
XX
DE
XX
XX
KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX
OS Homo sapiens.
XX
XX WO200047740-A2.
XX
XX PD 17-AUG-2000.
XX
XX PF 11-FEB-2000; 2000WO-US03653.
XX
XX PR 12-FEB-1999; 99US-0119906.
XX
XX PR 18-NOV-1999; 99US-0166271.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Boyle WJ, Hsu H;
XX
XX DR WPI; 2000-558217/51.
XX
XX PT Novel polypeptides comprising tumour necrosis factor ligand family
XX proteins, useful for treating inflammatory and immune disorders, e.g.
XX rheumatoid arthritis -
XX
XX PS Claim 14; Fig 9; 71pp; English.
XX
XX CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
XX specification describes an AGP-3 polypeptide, which is TNF ligand
XX family member. AGP-3 is a type II transmembrane protein, and is a
XX potent B cell stimulatory factor. Expression of AGP-3 correlates to
XX increases in the number of B cells and immunoglobulins produced.
XX AGP-3 proteins, antibodies, and nucleic acids may be used to treat
XX inflammatory and immune disorders, e.g. rheumatoid arthritis,
XX Crohn's disease, lupus and graft versus host disease. The nucleic
XX acids may be used to regulate the expression of an AGP-3 related
XX protein. The AGP-3 proteins, antibodies and nucleic acids are also
XX useful for the detection of AGP-3 agonists, antagonists and
XX characterizing interactions with AGP-3 related proteins.
XX
SQ Sequence 143 AA;

Query Match 60.7%; Score 741; DB 21; Length 143;
Best Local Similarity 99.3%; Pred. No. 1.9e-72;
Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 RAFPKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOPPGLYFIICQLQFLVQC 151
Db 1 rapfkswaylqvakhlnktlswnkdgilhgvryqdgndvlgvpglyfiicqlqflvqc 60
QY 152 PNNVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLSQLLDYLVQVNTTISVNDTF 211
Db 61 pnnsvdliklellinkhikqalvtvcesgmqtkhvyqnlsqlldylqvnttisvndtf 120
QY 212 QYIDTSTFPLENVLSIFLYSNSD 234
Db 121 qyidststfplenvlsiflysnsd 143

RESULT 6
AAB08277
ID AAB08277 standard; Protein; 143 AA.
XX

AC AAB08277;
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of a mouse TNF ligand CD30L.
XX
KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX
OS Mus sp.
XX
XX WO200047740-A2.
XX
XX PD 17-AUG-2000.
XX
XX PF 11-FEB-2000; 2000WO-US03653.
XX
XX PR 12-FEB-1999; 99US-0119906.
XX
XX PR 18-NOV-1999; 99US-0166271.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Boyle WJ, Hsu H;
XX
XX DR WPI; 2000-558217/51.
XX
XX PT Novel polypeptides comprising tumour necrosis factor ligand family
XX proteins, useful for treating inflammatory and immune disorders, e.g.
XX rheumatoid arthritis -
XX
XX PS Claim 14; Fig 9; 71pp; English.
XX
XX CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
XX specification describes an AGP-3 polypeptide, which is TNF ligand
XX family member. AGP-3 is a type II transmembrane protein, and is a
XX potent B cell stimulatory factor. Expression of AGP-3 correlates to
XX increases in the number of B cells and immunoglobulins produced.
XX AGP-3 proteins, antibodies, and nucleic acids may be used to treat
XX inflammatory and immune disorders, e.g. rheumatoid arthritis,
XX Crohn's disease, lupus and graft versus host disease. The nucleic
XX acids may be used to regulate the expression of an AGP-3 related
XX protein. The AGP-3 proteins, antibodies and nucleic acids are also
XX useful for the detection of AGP-3 agonists, antagonists and
XX characterizing interactions with AGP-3 related proteins.
XX
SQ Sequence 143 AA;

Query Match 49.8%; Score 608; DB 21; Length 143;
Best Local Similarity 78.0%; Pred. No. 5.1e-58;
Matches 110; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

QY 94 PFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOPPGLYFIICQLQFLVQC 153
Db 3 pskkswaylqvakhlnktlswnkdgilhgvryqdgndvlgvpglyfiicqlqflvqc 62
QY 154 NSVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLSQLLDYLVQVNTTISVNDTF 213
Db 63 hsvdltlqllnslkklktlvtvcesgvskniyqnlsqlldylqvnttisvndtf 122
QY 214 IDTSTFPLENVLSIFLYSNSD 234
Db 123 vdtstfplenvlsiflysnsd 143

RESULT 7
AAB08357
ID AAB08357 standard; Protein; 279 AA.
XX
XX AAB08357;
XX

DE Mouse Fas ligand (partial sequence).

KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;

KW Fas cell surface antigen; Fas-L; mouse.

XX Mus musculus.

XX WO9513293-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-JP01899.

XX 18-OCT-1994; 94JP-0278378.

XX 10-NOV-1993; 93JP-0305975.

XX 13-DEC-1993; 93JP-0342526.

XX 18-MAR-1994; 94JP-0074344.

XX 08-JUL-1994; 94JP-0180955.

XX 07-SEP-1994; 94JP-0239363.

XX (MOCH) MOCHIDA PHARM CO LTD.

XX (OSAB-) OSAKA BIOSCIENCE INST.

XX Nagata S, Nakamura N, Suda T, Takahashi T;

XX WPI; 1995-194031/25.

XX N-PSDB; AAQ99497.

XX Peptide which binds to Fas antigen, and antibody reactive with it

XX for treatment and diagnosis of viral or auto:immune diseases

XX Claim 10; Page 221-222; 300pp; Japanese.

XX Fas ligands or active fragments able to induce apoptosis in cells

XX which express the Fas cell surface antigen are claimed. The

XX proteins are isolated from human, rat and mouse sources. The present

XX sequence represents part of the mouse Fas ligand.

XX Sequence 138 AA;

Query Match 8.7%; Score 106; DB 16; Length 138;

Best Local Similarity 25.2%; Pred. No. 0.0014;

Matches 31; Conservative 22; Mismatches 46; Indels 24; Gaps 4;

QY 97 KSWAYLQVAKHLNKTLSWKNK---DGILHGVRVYQDGNLVIQFPGLYFIICQLQFLVQ-CP 152

DB 1 rsvahltgnphrsiplewedytgatllsgvkvkkgglvlnetglyfvyvskvyfrgqscn 60

153 NNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTRHVVYQNLNQ 192

61 nqpinhkvmynskypedvlvimeekrlvnyctgtgqiwahssylgavfnltsadhlvnynsq 120

QY 193 FLL 195

DB 121 lsl 123

RESULT 12

AAR79067

ID AAR79067 standard; Protein; 137 AA.

XX AC AAR79067;

XX 22-FEB-1996 (first entry)

DT Mouse Fas ligand (partial sequence).

DE Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;

KW Fas cell surface antigen; Fas-L; mouse.

XX Mus musculus.

PN WO9513293-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-JP01899.

XX 18-OCT-1994; 94JP-0278378.

XX 10-NOV-1993; 93JP-0305975.

XX 13-DEC-1993; 93JP-0342526.

XX 18-MAR-1994; 94JP-0074344.

XX 08-JUL-1994; 94JP-0180955.

XX 07-SEP-1994; 94JP-0239363.

XX (MOCH) MOCHIDA PHARM CO LTD.

XX (OSAB-) OSAKA BIOSCIENCE INST.

XX Nagata S, Nakamura N, Suda T, Takahashi T;

XX WPI; 1995-194031/25.

XX N-PSDB; AAQ99496.

XX Peptide which binds to Fas antigen, and antibody reactive with it

XX for treatment and diagnosis of viral or auto:immune diseases

XX Claim 9; Page 219-221; 300pp; Japanese.

XX Fas ligands or active fragments able to induce apoptosis in cells

XX which express the Fas cell surface antigen are claimed. The

XX proteins are isolated from human, rat and mouse sources. The present

XX sequence represents part of the mouse Fas ligand.

XX Sequence 137 AA;

Query Match 8.5%; Score 104; DB 16; Length 137;

Best Local Similarity 25.4%; Pred. No. 0.0023;

Matches 31; Conservative 21; Mismatches 46; Indels 24; Gaps 4;

QY 98 SWAYLQVAKHLNKTLSWKNK---DGILHGVRVYQDGNLVIQFPGLYFIICQLQFLVQ-CPN 153

DB 1 svahltgnphrsiplewedytgatllsgvkvkkgglvlnetglyfvyvskvyfrgqscn 60

QY 154 NSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTRHVVYQNLNQ 193

DB 61 qpinkhvmynskypedvlvimeekrlvnyctgtgqiwahssylgavfnltsadhlvnynsq 120

QY 194 LL 195

DB 121 sl 122

RESULT 13

AAR77282

ID AAR77282 standard; Protein; 279 AA.

XX AC AAR77282;

XX 05-DEC-1995 (first entry)

DT Mouse Fas-L protein.

DE Fas ligand; Fas-L; cell surface protein; autoimmune disease;

KW self-tolerance.

XX Mus sp.

XX Key Location/Qualifiers

FT Domain 1..78

FT Domain /label= Cytoplasmic_domain

FT Domain 79..103

FT Domain /label= Transmembrane_domain

FT Domain 104..279

FT Domain /label= Extracellular_domain

XX WO9518819-A.
 XX 13-JUL-1995.
 XX 06-JAN-1995; 95WO-US00362.
 XX 01-FEB-1994; 94US-0190559.
 XX 07-JAN-1994; 94US-0179138.
 XX (IMV) IMMUNEX CORP.
 XX Goodwin RG;
 XX WPI; 1995-255032/33.
 XX N-PSDB; AAQ91312.
 XX Human and murine DNA encoding ligand(s) binding to cell surface protein
 XX Fas - useful for studying auto-immune disorder(s) and development of
 XX self-tolerance.
 XX Disclosure; Page 29-30; 38pp; English.
 XX A cDNA library prep'd. from mouse peripheral blood lymphocyte mRNA was
 XX screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
 XX An isolated clone (AAQ91312) encoded mouse Fas-L.
 XX Sequence 279 AA;
 SQ
 Query Match 8.4%; Score 102; DB 16; Length 279;
 Best Local Similarity 22.9%; Pred. NO. 0.011;
 Matches 39; Conservative 28; Mismatches 57; Indels 46; Gaps 6;
 QY 52 FTVATIMVLVWRTDIPNSPDVPLKGGNCSEDLILCRAPFKKSWAYLQVAKHLNKT 111
 DB 115 ftnqslkvsfekaipstpe-----kkep--rsvahltgnphrsi 156
 QY 112 KLSWNK---DGLHGVRYQDGNLVIOFPGLYFIICQLQFLVQ-CPNNSVDLKLELLINKH 167
 DB 157 plwedtygtalisgvykkgglinetglyfvyyskvyfgrgscnqplnhkvymrnsky 216
 QY 168 IKKQALVTVCESGM-----QTKHVVYQNLQSFLL 195
 DB 217 --pedivlmeekrlnyftgtgiwahssyigavfnltsadhlyvnisqlsl 264
 RESULT 14
 ID AAW48953 standard; Protein; 268 AA.
 XX AAW48953;
 XX 23-SEP-1998 (first entry)
 XX Non-cleavable Fas ligand 1306142 deletion mutin.
 XX Non-cleavable Fas ligand 1306142 deletion mutin; Fas; erythematosis;
 XX gene therapy; autoimmune disease; multiple sclerosis;
 XX rheumatoid arthritis; myasthenia gravis; transplant rejection;
 XX glomerulonephritis.
 XX Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Region 1..129
 XX /note= "represents residues 1-129 of the wild-type
 XX Fas ligand"
 XX Region 130..268
 XX /note= "represents residues 143-281 of the
 XX wild-type Fas ligand"

PN WO9821232-A2.
 XX 22-MAY-1998.
 XX 13-NOV-1997; 97WO-US20864.
 XX 12-NOV-1997; 97US-0968686.
 XX 13-NOV-1996; 96US-0030871.
 XX 10-FEB-1997; 97US-0039972.
 XX (CHIR) CHIRON CORP.
 XX Chu K;
 XX WPI; 1998-297861/26.
 XX N-PSDB; AAV32622.
 XX New DNA encoding Fas ligand agonist including, e.g. deletion -
 XX useful for, e.g. treating auto-immune diseases or transplant
 XX rejection
 XX Claim 4; Pages 62-63; 72pp; English.
 XX The present sequence represents a non-cleavable Fas ligand 1306142
 XX deletion mutin. Fas ligand deletion mutin can be expressed in
 XX cells transfected with the DNA (AAV32622) coding for the mutant protein.
 XX These cells, expressing the mutant Fas ligand in a non-cleavable form,
 XX are claimed to be useful in vitro to identify cells that express Fas
 XX and, in vivo or in vitro, for reducing proliferation of Fas-expressing
 XX cells. The DNA encoding the Fas ligand mutant is claimed to be
 XX useful in gene therapy procedures and for the treatment of autoimmune
 XX diseases, e.g. multiple sclerosis, erythematosis, rheumatoid arthritis,
 XX glomerulonephritis, myasthenia gravis and transplant rejection.
 XX Sequence 268 AA;
 SQ
 Query Match 8.0%; Score 97; DB 19; Length 268;
 Best Local Similarity 22.4%; Pred. NO. 0.035;
 Matches 45; Conservative 27; Mismatches 55; Indels 74; Gaps 9;
 QY 68 IPNSPDVNPVL-----KGCNCEDELILCIL-----KRA 93
 DB 54 lpppppppplpplpplpklkrghnstg-lclilvmfmvalvglgmfglqlkela 112
 QY 94 PFKXSWAYLQVAKHLNKT-----LSWNKD-GI--LHGVRVYQDGNLVIOF 135
 DB 113 elrestsqmhtassleklrkvahltgksnrsrsmplewedygvlslgvykkggllvine 172
 QY 136 PGLYFIICQLQFLVQ-CPNNSVDLKLELLINKH-----IKKQALVTVCESGM----- 181
 DB 173 tglyfvyyskvyfgrgscnqplshkvymrnskyppqdlvmmeqkmnsycttgqmwarsyl 232
 QY 182 -----QTKHVVYQNLQSFLL 195
 DB 233 gavfnltsadhlyvnvselsl 253
 RESULT 15
 ID AAW48954 standard; Protein; 265 AA.
 XX AAW48954;
 XX 23-SEP-1998 (first entry)
 XX Non-cleavable Fas ligand 1306145 deletion mutin.
 XX Non-cleavable Fas ligand 1306145 deletion mutin; Fas; erythematosis;
 XX gene therapy; autoimmune disease; multiple sclerosis;
 XX rheumatoid arthritis; myasthenia gravis; transplant rejection;
 XX glomerulonephritis.
 XX

Search completed: January 22, 2002, 08:21:17
Job time: 302 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:21:18 ; Search time 78.06 Seconds
(without alignments)
204.019 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPVAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYSNSD 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
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15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	AA45007	Sequence encoded b
2	1118	100.0	234	AA45009	Sequence encoded b
3	814.5	72.9	220	AA45006	Sequence encoded b
4	814.5	72.9	239	AA45008	Sequence encoded b
5	741	66.3	143	AA45007	Amino acid sequenc
6	608	54.4	143	AA45007	Amino acid sequenc
7	115	10.3	279	AA45007	Mouse Fas ligand.
8	112	10.0	179	AA45009	Mouse Fas ligand (
9	112	10.0	279	AA45008	Mouse Fas ligand.
10	108	9.7	143	AA45006	Amino acid sequenc
11	106	9.5	138	AA45008	Mouse Fas ligand (

12	104	9.3	137	16	AA45007	Mouse Fas ligand (
13	102	9.1	279	16	AA45007	Mouse Fas-L protei
14	97	8.7	268	19	AA45009	Non-cleavable Fas
15	96.5	8.6	265	19	AA45009	Non-cleavable Fas
16	95	8.5	180	18	AA45007	FasL/Lt-alpha hybr
17	94.5	8.5	281	22	AA45007	Human Fas ligand p
18	93	8.3	216	19	AA45007	Hybrid alpha-1-thy
19	92	8.2	378	18	AA45007	Human Fas-Ligand-I
20	91.5	8.2	252	22	AA45008	FasL fusion constr
21	91.5	8.2	261	20	AA45009	Fas ligand (FasL)
22	91.5	8.2	281	21	AA45007	Human Fas ligand (
23	91.5	8.2	376	21	AA45008	Secreted modified
24	91	8.1	159	22	AA45007	FasL fusion constr
25	91	8.1	258	20	AA45007	Human Fas ligand d
26	90.5	8.1	145	18	AA45008	Human Fas-Ligand f
27	90.5	8.1	151	18	AA45007	Human Fas ligand (
28	90.5	8.1	178	16	AA45008	C-terminally delet
29	90.5	8.1	179	16	AA45009	Human Fas ligand (
30	90.5	8.1	179	18	AA45007	Fas ligand. Homo
31	90.5	8.1	213	22	AA45007	FasL fusion constr
32	90.5	8.1	213	22	AA45007	FasL fusion constr
33	90.5	8.1	271	20	AA45007	Fas ligand (FasL)
34	90.5	8.1	277	20	AA45007	Fas ligand (FasL)
35	90.5	8.1	277	20	AA45007	Human Fas ligand d
36	90.5	8.1	281	16	AA45007	Human Fas-L protei
37	90.5	8.1	281	16	AA45007	Human Fas ligand.
38	90.5	8.1	281	17	AA45007	Human Fas ligand d
39	90.5	8.1	281	17	AA45007	Human Fas ligand.
40	90.5	8.1	281	18	AA45007	Human Fas ligand.
41	90.5	8.1	281	19	AA45007	Human Fas ligand.
42	90.5	8.1	281	19	AA45007	Fas Ligand. Mamma
43	90.5	8.1	281	20	AA45007	Wild type Fas liga
44	90.5	8.1	281	20	AA45007	Human Fas ligand d
45	90.5	8.1	281	20	AA45007	Human Fas ligand (

ALIGNMENTS

RESULT 1
AA45007
ID AA45007 standard; Protein; 215 AA.
AC AA45007;
XX
XX
DT 19-JUN-1994 (first entry)
XX
DE Sequence encoded by a human CD30-L cDNA clone.
XX
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 22..43
FT /label= transmembrane
XX
PN WO9324135-A.
XX
PD 09-DEC-1993.
XX
PF 25-MAY-1993; 93WO-US04926.
XX
PR 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.
PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.
 DR N-PSDB; AAQ53536.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 XX Claim 15; Figure 5a; 59pp; English.
 PS
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
 CC This cDNA can then be used as a probe to screen a human PBL cDNA
 CC library to obtain cDNA encoding human CD30-L.
 XX
 XX Sequence 215 AA;
 SQ
 Query Match 100.0%; Score 1118; DB 14; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.2e-116;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
 DB 1 mhvpagsvashlgttsrsyfyttatlalclvftvatimlvvqrdtsipnsdpnvpk 60
 QY 61 GNCSEDLILCKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOFPGLY 120
 DB 61 gncsedlilckrapfkkswaylqvakhlnktlswknkgilhvryqdglnlviofpgly 120
 QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMQTKHVVQNLSQFLDYLQ 180
 DB 121 fiicqlqlvqcpnnsvdllkllinkhikkqalvtvcesgmqtkkhvynlsqfldylq 180
 QY 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYNSD 215
 DB 181 vnttisvnnvdtfgyidstfplenvlsiflynsd 215
 RESULT 2
 AAR45009
 ID AAR45009 standard; Protein; 234 AA.
 XX
 XX AAR45009;
 XX
 XX 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a human CD30-L cDNA clone
 DE encoding additional N-terminal amino acids.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 41..62
 FT /label= Transmembrane
 XX
 PN W09324135-A.
 PD
 XX 09-DEC-1993.
 XX
 PF 25-MAY-1993; 93WO-US04926.
 XX
 XX 26-MAY-1992; 92US-0889717.
 PR 02-JUN-1992; 92US-0892459.
 PR

PR 15-JUN-1992; 92US-0899660.
 PR 01-JUL-1992; 92US-0907224.
 PR 27-OCT-1992; 92US-0966775.
 XX
 PA (IMNV) IMMUNEX CORP.
 XX
 XX Armitage RJ, Goodwin RG, Smith CA;
 XX
 DR WPI; 1993-405417/50.
 DR N-PSDB; AAQ53538.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 XX Claim 15; Figure 7a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
 CC (AAQ53538). This cDNA can then be used as a probe to screen a human PBL
 CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
 CC anchored PCR technique was employed to isolate CD30-L human and murine
 CC clones containing an additional 19 N-terminal amino acid sequence
 CC (AAQ53537, AAQ53538).
 XX
 XX Sequence 234 AA;
 SQ
 Query Match 100.0%; Score 1118; DB 14; Length 234;
 Best Local Similarity 100.0%; Pred. No. 2.5e-116;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
 DB 20 mhvpagsvashlgttsrsyfyttatlalclvftvatimlvvqrdtsipnsdpnvpk 79
 QY 61 GNCSEDLILCKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOFPGLY 120
 DB 80 gncsedlilckrapfkkswaylqvakhlnktlswknkgilhvryqdglnlviofpgly 139
 QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMQTKHVVQNLSQFLDYLQ 180
 DB 140 fiicqlqlvqcpnnsvdllkllinkhikkqalvtvcesgmqtkkhvynlsqfldylq 199
 QY 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYNSD 215
 DB 200 vnttisvnnvdtfgyidstfplenvlsiflynsd 234
 RESULT 3
 AAR45006
 ID AAR45006 standard; Protein; 220 AA.
 XX
 XX AAR45006;
 XX
 XX 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a murine CD30-L cDNA clone.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Acomys cahirinus.
 XX
 FH Key Location/Qualifiers
 FT Region 28..48
 FT /label= transmembrane
 FT

```
XX PN WO9324135-A.
XX PD
XX PF 09-DEC-1993.
XX PP 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX PI WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53535.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 3a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cDNA library prepd. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX CC This cDNA can then be used as a probe to screen a human PBL cDNA
XX CC library to obtain cDNA encoding human CD30-L.
XX SQ Sequence 220 AA;
Query Match 72.9%; Score 814.5; DB 14; Length 220;
Best Local Similarity 70.6%; Pred. No. 1.5e-82;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
QY 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 54
DB 1 mqvqpgsvasprwstrprwstrsrsfyfisttal-vclvvavaillvqvkkdstpttte 59
QY 55 NVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKDGILHGVRVQDGNLVI 114
DB 60 kaplkgncsedlftclktspkkskswaylqvskhlnntklswnedgtihglyqdggnliv 119
QY 115 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGMOVKHYQNLVSQF 174
DB 120 qfpglyfivcqlqflvqcshsvdltqlqllnskikktqlvtvcsgsvqskniyqnlvsqf 179
QY 175 LDYLVQVNTTISVNDVTFQYIDTSTFPLENVLSIFLYSNSD 215
DB 180 llhylvqvnstisvrvdnfqyvdntnfpldnvlsflysssd 220
RESULT 4
AAR45008
ID AAR45008 standard; Protein; 239 AA.
XX AC AAR45008;
XX DT 19-JUN-1994 (first entry)
XX DE Sequence encoded by a murine CD30-L cDNA clone
XX DE encoding additional N-terminal amino acids.
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
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KW CD30 ligand; CD30-L; TNF; NGF.
XX OS Acomys cahirinus.
XX FH Key Location/Qualifiers
XX FT Region 47..67
XX FT /label= Transmembrane
XX XX
XX PN WO9324135-A.
XX PD 09-DEC-1993.
XX PP 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX PI WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53537.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 6a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cDNA library prepd. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX CC anchored PCR technique was employed to isolate CD30-L human and murine
XX CC clones containing an additional 19 N-terminal amino acid sequence
XX CC (AAQ53537, AAQ53538).
XX SQ Sequence 239 AA;
Query Match 72.9%; Score 814.5; DB 14; Length 239;
Best Local Similarity 70.6%; Pred. No. 1.7e-82;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
QY 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 54
DB 20 mqvqpgsvasprwstrprwstrsrsfyfisttal-vclvvavaillvqvkkdstpttte 78
QY 55 NVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKDGILHGVRVQDGNLVI 114
DB 79 kaplkgncsedlftclktspkkskswaylqvskhlnntklswnedgtihglyqdggnliv 138
QY 115 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGMOVKHYQNLVSQF 174
DB 139 qfpglyfivcqlqflvqcshsvdltqlqllnskikktqlvtvcsgsvqskniyqnlvsqf 198
QY 175 LDYLVQVNTTISVNDVTFQYIDTSTFPLENVLSIFLYSNSD 215
DB 199 llhylvqvnstisvrvdnfqyvdntnfpldnvlsflysssd 239
RESULT 5
AAB08276
```

ID AAB08276 standard; Protein; 143 AA.
 AC AAB08276;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a human TNF ligand CD30L.
 XX
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200047740-A2.
 XX
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-US03653.
 XX
 PR 12-FEB-1999; 99US-0119906.
 XX
 PR 18-NOV-1999; 99US-0166271.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Hsu H;
 XX
 DR WPI; 2000-558217/51.
 XX
 DR Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 PT
 PS Claim 14; Fig 9; 7lpp; English.
 XX
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 XX
 SQ Sequence 143 AA;

 Query Match 66.3%; Score 741; DB 21; Length 143;
 Best Local Similarity 99.3%; Pred. No. 1.3e-74;
 Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 73 RAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRVYQDGNLVIOFPGLYFIICQLQFLVQC 132
 Db 1 rapfkkswaylvakhlntklswnkdgilhgvryqdgndlviofpglyfiicqlqlvqc 60

 QY 133 PNNVDKLELLINKHIKKOALVTVCESGMQTKHVYONLSQFLDYLQVNTTISVNVDTF 192
 Db 61 pnnsvdklellinkhikqalvtvcsgmqtkhvygnlsqfildylqvmnttisvndtf 120

 QY 193 QYIDTSTFPLENVLSIFLYSNSD 215
 Db 121 qyidstfplenvlsiflysnsd 143

 RESULT 6
 AAB08277
 ID AAB08277 standard; Protein; 143 AA.
 XX

AC AAB08277;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a mouse TNF ligand CD30L.
 XX
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX
 OS Mus sp.
 XX
 PN WO200047740-A2.
 XX
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-US03653.
 XX
 PR 12-FEB-1999; 99US-0119906.
 XX
 PR 18-NOV-1999; 99US-0166271.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Hsu H;
 XX
 DR WPI; 2000-558217/51.
 XX
 DR Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 PT
 PS Claim 14; Fig 9; 7lpp; English.
 XX
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 XX
 SQ Sequence 143 AA;

 Query Match 54.4%; Score 608; DB 21; Length 143;
 Best Local Similarity 78.0%; Pred. No. 8.5e-60;
 Matches 110; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

 QY 75 PFKKSWAYLQVAKHLNKTLSWKNKGILHGVRVYQDGNLVIOFPGLYFIICQLQFLVQC 134
 Db 3 pskkswaylvakhlntklswnkdgilhgvryqdgndlviofpglyfiicqlqlvqc 62

 QY 135 NSVDKLELLINKHIKKOALVTVCESGMQTKHVYONLSQFLDYLQVNTTISVNVDTF 194
 Db 63 hsdvdtlqlilnskikqlvtvcsgvqskniysqfildylqvnstisvrvdnfy 122

 QY 195 IDTSTFPLENVLSIFLYSNSD 215
 Db 123 vdtstfplenvlsiflysnsd 143

 RESULT 7
 AAB88357
 ID AAB88357 standard; Protein; 279 AA.
 XX
 AC AAB88357;
 XX

DE	Mouse Fas ligand (partial sequence).
XX	
KW	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW	Fas cell surface antigen; Fas-L; mouse.
XX	
OS	Mus musculus.
XX	
PN	WO9513293-A1.
XX	
PD	18-MAY-1995.
XX	
PF	10-NOV-1994; 94WO-JP01899.
XX	
PR	18-OCT-1994; 94JP-0278378.
PR	10-NOV-1993; 93JP-0305975.
PR	13-DEC-1993; 93JP-0342526.
PR	18-MAR-1994; 94JP-0074344.
PR	08-JUL-1994; 94JP-0180955.
PR	07-SEP-1994; 94JP-0233963.
XX	
PA	(MOCH) MOCHIDA PHARM CO LTD.
PA	(OSAB-) OSAKA BIOSCIENCE INST.
XX	
XX	Nagata S, Nakamura N, Suda T, Takahashi T;
DR	WPI; 1995-194031/25.
DR	N-PSDB; AAQ99497.
XX	
PT	Peptide which binds to Fas antigen, and antibody reactive with it -
PT	for treatment and diagnosis of viral or auto:immune diseases
XX	
PS	Claim 10; Page 221-222; 300pp; Japanese.
XX	
CC	Fas ligands or active fragments able to induce apoptosis in cells
CC	which express the Fas cell surface antigen are claimed. The
CC	proteins are isolated from human, rat and mouse sources. The present
CC	sequence represents part of the mouse Fas ligand.
XX	
SQ	Sequence 138 AA;
	Query Match 9.5%; Score 106; DB 16; Length 138;
	Best Local Similarity 25.2%; Pred. No. 0.00072;
	Matches 31; Conservative 22; Mismatches 46; Indels 24; Gaps
QY	78 KSWAYLOVAXHLNKTKLSWNK---DCILHGVRVQDGNLVQFPGLYFIICQLQFLVQ-CP 133
Db	1 rsvahltgnphrsisplewedtygtalisgvkykkgglvinetglyfvyskvyfgrgscn 60
	134 NNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTKHVVYONLSQ 173
	61 nqpnkhkvmrnsypedivlmeekrlnycctgqlwahhsyigavfnlttsadhllyvnisq 120
QY	174 FLL 176
Db	121 lsl 123
RESULT 12	
AAR79067	
ID	AAR79067 standard; Protein; 137 AA.
XX	
AC	AAR79067;
XX	
DT	22-FEB-1996 (first entry)
XX	
XX	Mouse Fas ligand (partial sequence).
XX	
KW	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW	Fas cell surface antigen; Fas-L; mouse.
XX	
OS	Mus musculus.
XX	

XX WO9518819-A.
 PN 13-JUL-1995.
 XX 06-JAN-1995; 95WO-US00362.
 XX 01-FEB-1994; 94US-0190559.
 PR 07-JAN-1994; 94US-0179138.
 XX (IMMUNEX CORP.
 PA Goodwin RG;
 XX WPI; 1995-255032/33.
 DR N-PSDB; AAQ91312.
 XX Human and murine DNA encoding ligand(s) binding to cell surface protein
 Fas - useful for studying auto-immune disorder(s) and development of
 self-tolerance.
 XX Disclosure; Page 29-30; 38pp; English.
 PS A cDNA library prep'd. from mouse peripheral blood lymphocyte mRNA was
 CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
 CC An isolated clone (AAQ91312) encoded mouse Fas-L.
 XX Sequence 279 AA;
 SQ

Query Match 9.1%; Score 102; DB 16; Length 279;
 Best Local Similarity 22.9%; Pred. No. 0.0055;
 Matches 39; Conservative 28; Mismatches 57; Indels 46; Gaps 6;
 QY 33 FTVATIMVLVORTDIPNSPDVPLKGGNCSEDLILKRAPFKKSWAYLQVAKHLNKT 92
 Db 115 fnqslkvsfekqanptse-----kkep--rsvahltgnphrsi 156
 QY 93 KLSWNK---DGLIHGVRYODGNLVIQFPGLYFTICQLFLVQ-CPNNSVDLKLLELNKH 148
 Db 157 plewedtygtalisgvykkggvlvnetglyfvyksvfyrgscnqpinhkvmrnksy 216
 QY 149 IKKQALVTVCESGM-----QTRHVVONLSQFL 176
 Db 217 --pedivlmeekrlnyfttggivahssylgavfnltsadhlyvnisqlsl 264

RESULT 14
 AAW48953
 ID AAW48953 standard; Protein; 268 AA.
 XX AAW48953;
 AC AAW48953;
 XX 23-SEP-1998 (first entry)
 DT Non-cleavable Fas ligand 1306142 deletion mutain.
 DE Non-cleavable Fas ligand 1306142 deletion mutain; Fas; erythematosis;
 KW gene therapy; autoimmune disease; multiple sclerosis;
 KW rheumatoid arthritis; myasthenia gravis; transplant rejection;
 KW glomerulonephritis.
 OS Homo sapiens.
 OS Synthetic.
 XX Key
 FH Region
 FT Location/Qualifiers
 FT 1..129
 FT /note= "represents residues 1-129 of the wild-type
 FT Fas ligand"
 FT 130..268
 FT /note= "represents residues 143-281 of the
 FT wild-type Fas ligand"
 XX

PN WO9821232-A2.
 XX 22-MAY-1998.
 PD 13-NOV-1997; 97WO-US20864.
 XX 12-NOV-1997; 97US-0968686.
 PR 13-NOV-1996; 96US-0030871.
 PR 10-FEB-1997; 97US-0039972.
 XX (CHIRON) CHIRON CORP.
 PA Chu K;
 XX WPI; 1998-297861/26.
 DR N-PSDB; AAV32622.
 XX New DNA encoding Fas ligand agonist including, e.g. deletion -
 PT useful for, e.g. treating auto-immune diseases or transplant
 PT rejection
 PT Claim 4; Pages 62-63; 72pp; English.
 PS The present sequence represents a non-cleavable Fas ligand 1306142
 CC deletion mutain. Fas ligand deletion mutain can be expressed in
 CC cells transfected with the DNA (AAV32622) coding for the mutant protein.
 CC These cells, expressing the mutant Fas ligand in a non-cleavable form,
 CC are claimed to be useful in vitro to identify cells that express Fas
 CC and, in vivo or in vitro, for reducing proliferation of Fas-expressing
 CC cells. The DNA encoding the Fas ligand mutant is claimed to be
 CC useful in gene therapy procedures and for the treatment of autoimmune
 CC diseases, e.g. multiple sclerosis, erythematosis, rheumatoid arthritis,
 CC glomerulonephritis, myasthenia gravis and transplant rejection.
 XX Sequence 268 AA;
 SQ

Query Match 8.7%; Score 97; DB 19; Length 268;
 Best Local Similarity 22.4%; Pred. No. 0.019;
 Matches 45; Conservative 27; Mismatches 55; Indels 74; Gaps 9;
 QY 49 IPNSPDVPL-----KGCNSEDLLCIL-----KRA 74
 Db 54 lpppppppplplpplpkkrgnhstg-lclllvmfmvlvalvglgmfqihlqkela 112
 QY 75 PFKKSWAYLQVAKHLNKT-----LSWNKD-GI--LHGVRYODGNLVIQF 116
 Db 113 elrestsqmhtassleklrkvahltgksnrsrsmplewedtygvlisgvkykkggvlvne 172
 QY 117 PGLYFTICQLFLVQ-CPNNSVDLKLLELNKH-----IKKQALVTVCESGM----- 162
 Db 173 tglyfvyksvfyrgscnqnlplshkvmrnksykpqdlvmmeqkmnsycttgqmwarsyl 232
 QY 163 -----QTRHVVONLSQFL 176
 Db 233 gavfnltsadhlyvnvselsl 253

RESULT 15
 AAW48954
 ID AAW48954 standard; Protein; 265 AA.
 XX AAW48954;
 AC AAW48954;
 XX 23-SEP-1998 (first entry)
 DT Non-cleavable Fas ligand 1306145 deletion mutain.
 DE Non-cleavable Fas ligand 1306145 deletion mutain; Fas; erythematosis;
 KW gene therapy; autoimmune disease; multiple sclerosis;
 KW rheumatoid arthritis; myasthenia gravis; transplant rejection;
 KW glomerulonephritis.
 XX

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:22:26 ; Search time 39.95 Seconds
(without alignments)
121.107 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYNSD 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	US-08-225-989-23	Sequence 23, Appl
2	1118	100.0	215	US-08-570-923-23	Sequence 23, Appl
3	1118	100.0	215	US-08-580-014-23	Sequence 23, Appl
4	1118	100.0	215	US-09-079-785-23	Sequence 23, Appl
5	1118	100.0	234	US-08-225-989-8	Sequence 8, Appli
6	1118	100.0	234	US-08-570-923-8	Sequence 8, Appli
7	1118	100.0	234	US-08-580-014-8	Sequence 8, Appli
8	1118	100.0	234	US-09-079-785-8	Sequence 8, Appli
9	814.5	72.9	220	US-08-225-989-19	Sequence 19, Appl
10	814.5	72.9	220	US-08-570-923-19	Sequence 19, Appl
11	814.5	72.9	220	US-08-580-014-19	Sequence 19, Appl
12	814.5	72.9	220	US-09-079-785-19	Sequence 19, Appl
13	814.5	72.9	239	US-08-225-989-6	Sequence 6, Appli
14	814.5	72.9	239	US-08-570-923-6	Sequence 6, Appli
15	814.5	72.9	239	US-08-580-014-6	Sequence 6, Appli
16	814.5	72.9	239	US-09-079-785-6	Sequence 6, Appli
17	775	69.3	148	US-08-584-031-12	Sequence 12, Appl
18	592	53.0	125	US-08-225-989-20	Sequence 20, Appl
19	592	53.0	125	US-08-570-923-20	Sequence 20, Appl
20	592	53.0	125	US-08-580-014-20	Sequence 20, Appl
21	592	53.0	125	US-09-079-785-20	Sequence 20, Appl
22	447.5	40.0	130	US-08-225-989-21	Sequence 21, Appl
23	447.5	40.0	130	US-08-570-923-21	Sequence 21, Appl
24	447.5	40.0	130	US-08-580-014-21	Sequence 21, Appl
25	447.5	40.0	130	US-09-079-785-21	Sequence 21, Appl
26	274	24.5	52	US-09-369-494-17	Sequence 17, Appl
27	274	24.5	52	US-09-358-569D-15	Sequence 15, Appl

28 102 9.1 279 5 PCT-US95-00362-5 Sequence 5, Appli
29 92 8.2 378 3 US-08-630-172-21 Sequence 21, Appl
30 92 8.2 378 4 US-09-375-419-21 Sequence 21, Appl
31 91.5 8.1 376 3 US-08-751-512-8 Sequence 8, Appli
32 90.5 8.1 145 3 US-08-630-172-5 Sequence 5, Appli
33 90.5 8.1 145 4 US-09-375-419-5 Sequence 5, Appli
34 90.5 8.1 179 3 US-08-649-100-9 Sequence 9, Appli
35 90.5 8.1 281 2 US-08-810-453-2 Sequence 2, Appli
36 90.5 8.1 281 3 US-08-815-190A-2 Sequence 2, Appli
37 90.5 8.1 281 4 US-09-290-640-25 Sequence 25, Appl
38 90.5 8.1 281 4 US-09-479-524-3 Sequence 2, Appli
39 90.5 8.1 281 5 PCT-US95-00362-2 Sequence 2, Appli
40 90.5 8.1 287 3 US-08-815-190A-16 Sequence 16, Appl
41 90 8.1 141 4 US-09-286-529-22 Sequence 22, Appl
42 90 8.1 149 3 US-08-584-031-17 Sequence 17, Appl
43 86 7.7 158 1 US-07-994-469A-99 Sequence 99, Appl
44 85.5 7.6 309 1 US-08-236-918A-2 Sequence 2, Appli
45 85 7.6 161 1 US-07-994-469A-61 Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-08-225-989-23
; Sequence 23, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

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; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-23

Query Match 100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
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61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVIOFPGLY 120
Qy 121 FIICQLQFLVQCPNNSVDLKLLELNKHKIKKQALVTVCESGMOTKHVYQNLQSFLLDY 180
Db 121 FIICQLQFLVQCPNNSVDLKLLELNKHKIKKQALVTVCESGMOTKHVYQNLQSFLLDY 180
Qy 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215
Db 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215

/ RESULT 2
US-08-570-923-23
; Sequence 23, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-23

Query Match 100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVIOFPGLY 120
61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVIOFPGLY 120
Qy 121 FIICQLQFLVQCPNNSVDLKLLELNKHKIKKQALVTVCESGMOTKHVYQNLQSFLLDY 180
Db 121 FIICQLQFLVQCPNNSVDLKLLELNKHKIKKQALVTVCESGMOTKHVYQNLQSFLLDY 180
Qy 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215
Db 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215

RESULT 3
US-08-580-014-23
; Sequence 23, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:17:43 ; Search time 55.1 Seconds
(without alignments)
323.500 Million cell updates/sec

Title: US-09-628-126-8
Perfect score: 1220
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Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1220	100.0	234	2	CD30 ligand - huma
2	860.5	70.5	239	2	CD30 ligand - mouse
3	112	9.2	279	2	Fas ligand - mouse
4	108.5	8.9	809	2	hypothetical prote
5	96.5	7.9	234	1	tumor necrosis fac
6	94	7.7	235	2	tumor necrosis fac
7	94	7.7	547	2	rifampicin resista
8	90.5	7.4	281	2	Fas ligand - human
9	90	7.4	233	1	tumor necrosis fac
10	87.5	7.2	813	2	hypothetical prote
11	86.5	7.1	3512	2	CPY protein - midg
12	86	7.0	278	2	fes ligand - rat
13	85.5	7.0	309	2	4-LBB ligand - mou
14	85	7.0	235	1	tumor necrosis fac
15	84.5	6.9	232	1	tumor necrosis fac
16	84	6.9	287	2	methylenetetrahydr
17	83.5	6.8	234	1	tumor necrosis fac
18	83	6.8	636	2	hypothetical prote
19	83	6.8	1385	2	paraspinal crystal
20	82	6.7	513	2	hypothetical prote
21	82	6.7	1339	2	hypothetical prote
22	81.5	6.7	374	2	probable regulator
23	81.5	6.7	461	2	ID-myo-inositol-tr
24	81	6.6	233	1	tumor necrosis fac
25	81	6.6	547	2	hypothetical 61.6
26	81	6.6	1289	2	paraspinal crystal
27	80.5	6.6	434	1	ORF MSV157 hypothe
28	80.5	6.6	434	1	hypothetical prote
29	80.5	6.6	499	2	phosphoprotein pho

30	80	6.6	235	2	JU0029
31	79.5	6.5	233	1	S24642
32	79.5	6.5	5825	2	T12117
33	79	6.5	372	2	D64716
34	79	6.5	800	2	S53079
35	78.5	6.4	426	2	S64748
36	78.5	6.4	1130	2	T29089
37	78.5	6.4	1830	2	E82909
38	77.5	6.4	492	2	S42735
39	77.5	6.4	610	2	S71758
40	77.5	6.4	623	2	B96681
41	77.5	6.4	829	2	S72366
42	77	6.3	329	2	T28412
43	77	6.3	456	2	B96688
44	76.5	6.3	478	2	T27714
45	76.5	6.3	619	2	S54636

ALIGNMENTS

RESULT 1

A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, R.; Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <SMI>
A:Cross-references: GB:L09753; NID:g349277; PIDN:AAA74594.1; PID:g349278
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1220; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 5.7e-109;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDPLQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL	60
DB	1	MDPLQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL	60
QY	61	VVQRTDSTPNPDVPLKGGNCSEDLICILKRAPEKSWAYLQVAKHLNKTLSNWKDGI	120
DB	61	VVQRTDSTPNPDVPLKGGNCSEDLICILKRAPEKSWAYLQVAKHLNKTLSNWKDGI	120
QY	121	LHGVRDGNLVIFPPGLYFIICQLQFLVQCPNNSVDLKLKLLINKHKKQALVTVCSG	180
DB	121	LHGVRDGNLVIFPPGLYFIICQLQFLVQCPNNSVDLKLKLLINKHKKQALVTVCSG	180
QY	181	MOTRHVYONLSQFLDYLVQVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD	234
DB	181	MOTRHVYONLSQFLDYLVQVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD	234

RESULT 2

B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, R.; Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-239 <SMI>

A:Cross-references: GB:I09754; NID:g349288; PIDN:AAA74595.1; PID:g349289

A:Experimental source: strain 972h-; cosmid c1d4

C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 70.5%; Score 860.5; DB 2; Length 239;
Best Local Similarity 69.6%; Pred. No. 1.2e-74;
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

- QY 1 MDPELOALNGMAPPDGTAMHVPAGSVAS-----HLGTTSSRYFYLTATLALCLVFTV 54
Db 1 MEPELOAQSGCAPSPDPAMOVQPGSVASPMWRSTRPRMSTRSYFYLTATL-VCLVAV 59
QY 55 ATIMVLVVRTDIPSPNDVPLKGGNCSEDLILCRAPFKKSWAYLQVAKHLNKTLS 114
Db 60 AILVLVQKKDTPNTTEKAPLKGNCSEDLILCTKSTPKKSWAYLQVAKHLNKTLS 119
QY 115 WNKDGLHGVRYQDGLVIOFPGLYFIICQLQFLVOCNNVDLKLLELHKKHKKQALV 174
Db 120 WNEGDTGLIYQDGLVIOFPGLYFIVCQLQFLVOCNNHSDVLTQLLINSKIKKQTLV 179
QY 175 TVCESGMQTKHVYQNLQSLFDLVLQVNTTISVWVDTFOYIDTFFPLENVLSIFLYNSD 234
Db 180 TVCESGVQSKNIYQNLQSLFLLHVLQVNSTISVRVDFNQYVDNTFFPLDNVLSVFLSSD 239

RESULT 3
A53062

Fas ligand - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: A53062

R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994

A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in

A:Reference number: A53062; MUID:94185175

A:Accession: A53062

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-279 <YAK>

A:Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 9.2%; Score 112; DB 2; Length 279;
Best Local Similarity 22.6%; Pred. No. 0.0042;
Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;

QY 52 FTVATIMVLVVRTDIPSPNDVPLKGGNCSEDLILCRAPFKKSWAYLQVAKHLNKT 111
Db 115 FTNQSLKVSSEFKQIANPSPFSE-----KKEP--RSVAHLTGNPHRSI 156
QY 112 KLSWNK---DGLHGVRYQDGLVIOFPGLYFIICQLQFLVQ-CPNNSVDLKLLELHKKH 167
Db 157 PLEWEDTYGTALISGVYKKGGLVINETGLYFVYKVFYRGQSCNQPLNKHVYMRNSKY 216
QY 168 -----IKKQALVTVCESGM-----QTKHVYQNLQSL 195
Db 217 PEDLVLMEEKRLNYCTGTQIAWSSYLGAVFNLTSAHLVYNTSQLSL 264

RESULT 4
T38051

hypothetical protein SPAC1D4.10 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38051

R:Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1995

A:Reference number: Z21765

A:Accession: T38051

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-809 <LYE>

A:Cross-references: EMBL:Z69239; PIDN:CAA93219.1; GSPDB:GN00066; SPDB:SPAC1D4.10

A:Experimental source: strain 972h-; cosmid c1d4

C:Genetics:

A:Gene: SPDB:SPAC1D4.10

A:Map position: 1

A:Introns: 129/1

Query Match 8.9%; Score 108.5; DB 2; Length 809;
Best Local Similarity 22.6%; Pred. No. 0.034;
Matches 68; Conservative 39; Mismatches 101; Indels 93; Gaps 16;

QY 3 PGLQALNGMAPPGDT-----AMHVPAGSVASHLGTTSRYFYLTATL-----ALC 49
Db 128 PGFLLSLNDISEPGETGEASPFVLHGP--SEVHQFLLSSMRHYHTNVNLTVOGYTSAEA 185
QY 50 LVFT-----VATIMVLVVRT-----DSIPNSPDNVPLKG-----GNCSEDLIC 88
Db 186 PVFVDENICVTGVVSVLVKNSEFKRKHEINRGCTNARPLKEDRANTSPHWYSHVSNDSF 245
QY 89 ILKRAPPK-----KSWAYLQ--VAKHLNKTLSWNKD---GILHG-----V 124
Db 246 VVENAMYNTPAPLEPKPELFISYIVQSHPTPGKDAKAKSLGTLKGLDCGRLARGEVP 305
QY 125 RVQDNLVI-----QPPGLYFIICQLQFLVOCNNVDLKLLELHKKHKKQALVTVC 177
Db 306 TLENGKTYPREVIGPSIPGSSF-----FIHCNP---ELVIDLVLENHKNWNAKPKVC 356
QY 178 ESGMQTKHVYQN-----LSQF-----LLDYIQVNTTI-----SVNVDTFYIDTSTFP 220
Db 357 VHSVTPEVKNPRYQSWISSPSEVSHLIASTEVEVNEVINYPERSAVAIAIATLNLDSKVFP 416
QY 221 L 221
Db 417 L 417

RESULT 5
JQ1344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: JQ1344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis

A:Reference number: JQ1344; MUID:92084125

A:Accession: JQ1344

A:Molecule type: DNA

A:Residues: 1-234 <SU>

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 7.9%; Score 96.5; DB 1; Length 234;

Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;

QY 37 SYFYLTATLALCLVFTVATIMVLVVRTDIPSPNDVPLKGGNCSEDLILCRAPPK 96
Db 37 SFLLVAGATTTLFCLLH----FGVIGPQREQLPNAFQSI-----NPLAQTLSSSRTPSD 87

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:31:34 ; Search time 33.56 Seconds
(without alignments)
255.649 Million cell updates/sec

Title: US-09-628-126-8

Perfect score: 1220

Sequence: 1 MDPGLQALNGMPPGDTAM.....DTSTFPLENVLSIFLYNSND 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1220	100.0	234	1	TNF8_HUMAN	P32971 homo sapien
2	860.5	70.5	239	1	TNF8_MOUSE	P32972 mus musculus
3	112	9.2	279	1	FASL_MOUSE	P41047 mus musculus
4	108.5	8.9	809	1	YATA_SCHPO	Q10155 schizosacch
5	96.5	7.9	234	1	TNFA_HORSE	P29553 equus caball
6	94	7.7	233	1	TNFA_MACMU	P48094 macaca mula
7	94	7.7	235	1	TNFA_PERLE	P36939 peromyscus
8	92	7.5	233	1	TNFA_MACFA	P79337 macaca fasc
9	90.5	7.4	281	1	FASL_HUMAN	P48023 homo sapien
10	90	7.4	233	1	TNFA_PAPHU	O77510 papio hamad
11	90	7.4	233	1	TNFA_PAPSP	P33620 papio sp. (
12	86	7.0	278	1	FASL_RAT	P36940 rattus norv
13	85.5	7.0	309	1	1BL_MOUSE	P41274 mus musculus
14	85	7.0	233	1	TNFA_CANFA	P51742 canis famill
15	85	7.0	235	1	TNFA_MOUSE	P06804 mus musculus
16	85	7.0	1220	1	CSAC_BACTU	P56955 bacillus th
17	84.5	6.9	232	1	TNFA_PIG	P23563 sus scrofa
18	83.5	6.8	234	1	TNFA_SHEEP	P23383 ovis aries
19	83	6.8	1385	1	CSAA_BACUD	Q45760 bacillus th
20	81.5	6.7	461	1	IF3K_HUMAN	P23677 homo sapien
21	81	6.6	233	1	TNFA_HUMAN	P01375 homo sapien
22	81	6.6	233	1	TNFA_MARMO	O35734 marmota mon
23	81	6.6	541	1	YHXB_ECOLI	P42640 escherichia
24	81	6.6	1289	1	CSAB_ECOLI	Q45753 bacillus th
25	80.5	6.6	499	1	PP5_RAT	P53042 rattus norv
26	80	6.6	229	1	TNFA_CEREL	P51743 cervus elap
27	80	6.6	235	1	TNFA_RAT	P16599 rattus norv
28	79.5	6.5	233	1	TNFA_BOVIN	Q06599 bos taurus
29	79	6.5	800	1	PT11_YEAST	P08468 saccharomyc
30	78.5	6.4	424	1	TNFA_CAVPO	P51435 cavia porce
31	78.5	6.4	426	1	MMML_YEAST	P41800 saccharomyc
32	77.5	6.4	670	1	DD18_HUMAN	Q9nvp1 homo sapien
33	77.5	6.4	829	1	TOP1_XENLA	P41512 xenopus lae

34	76	6.2	479	1	PAP1_VACCC	P21079 vaccinia vi
35	76	6.2	982	1	MSHM_SARGL	O63852 sarcophyton
36	75.5	6.2	807	1	SUST_ARATH	P49040 arabidopsis
37	75	6.1	427	1	SYS_BUCAP	P81434 buchnera ap
38	75	6.1	499	1	PPP5_HUMAN	P53041 homo sapien
39	74.5	6.1	745	1	RNR_BUCAI	P57628 buchnera ap
40	74	6.1	459	1	IP3K_RAT	P17105 rattus norv
41	74	6.1	541	1	YHXB_ECO57	P58216 escherichia
42	74	6.1	851	1	NUD1_YEAST	P32336 saccharomyc
43	74	6.1	1064	1	CYAM_RAT	P26770 rattus norv
44	74	6.1	2136	1	YCF2_MARPO	P09975 marchantia
45	73.5	6.0	1178	1	PH81_YEAST	P17442 saccharomyc

ALIGNMENTS

RESULT 1	
TNF8_HUMAN	
ID	TNF8_HUMAN
AC	P32971
DT	01-OCT-1993 (Rel. 27, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN	TNFSF8 OR CD30LG OR CD30L.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=93313964; PubMed=8391931;
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrar T.,
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA	Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA	Falk B., Gimpson S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT	ligand defines an emerging family of cytokines with homology to
RT	TNF".
RL	Cell 73:1349-1360(1993).
CC	-!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC	T CELLS.
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC	-!- DATABASE: NAME=PRO; NOTE=CD guide CD153 entry;
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL: L09753; AAA74594.1; -
DR	PIR; A40710; A40710.
DR	MIM; 603875; -
DR	InterPro; IPR003638; TNF_8.
DR	InterPro; IPR000478; TNF_family.
DR	Pfam; PF00229; TNF; 1.
DR	ProDom; PD023087; TNF_8; 1.
DR	SMART; SM00207; TNF; 1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS00049; TNF_2; 1.
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT	DOMAIN 1 37
FT	TRANSMEM 38 62
FT	DOMAIN 63 234
FT	CARBOHYD 81 81
FT	CARBOHYD 109 109
FT	CARBOHYD 153 153
FT	-----
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT	EXTRACELLULAR (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 234 AA; 26017 MW; C65361568230581B CRC64;

Query Match 100.0%; Score 1220; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 8e-108; Indels 0; Gaps 0;
 Matches 234; Conservative 0; Mismatches 0;

QY 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSFYFLTATLALCLVFTVATIMVL 60
 DB 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSFYFLTATLALCLVFTVATIMVL 60

QY 61 VQRTSDIPNSPDNVLKGCNSEDLLCILKRAPFKKSWAYLQVAKHLNKTLSMNRDGI 120
 DB 61 VQRTSDIPNSPDNVLKGCNSEDLLCILKRAPFKKSWAYLQVAKHLNKTLSMNRDGI 120

QY 121 LHGVRVQDGNLVTFQPLGYFIICQLQFLVQCPNNSVDLKLLELNKHKQALVTCESG 180
 DB 121 LHGVRVQDGNLVTFQPLGYFIICQLQFLVQCPNNSVDLKLLELNKHKQALVTCESG 180

QY 181 MQTKHVQNLSQFLLDYLVQNTTISVNVDTFQXIDTSTFPLENVLSTFLYSNSD 234
 DB 181 MQTKHVQNLSQFLLDYLVQNTTISVNVDTFQXIDTSTFPLENVLSTFLYSNSD 234

RESULT 2
 TNF8_MOUSE
 ID TNF8_MOUSE STANDARD; PRT; 239 AA.
 AC P32972;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CD30 LIGAND (CD30-L).
 GN TNFSF8 OR CD30LG OR CD30L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
 Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
 Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
 Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
 "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
 ligand defines an emerging family of cytokines with homology to
 TNF.";
 RL Cell 73:1349-1360(1993).
 CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
 T CELLS.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L09754; AAA74595.1; -;
 DR PIR; B40710; B40710.
 DR MGD; MGI:88328; Tnfsf8.
 DR InterPro; IPR003638; TNF8.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD023087; TNF; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; P500251; TNF_1; 1.

DR PROSITE; P50049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 70.5%; Score 860.5; DB 1; Length 239;
 Best Local Similarity 69.6%; Pred. No. 6.1e-74;
 Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

QY 1 MDPGLQALNGMAPPDGTAMHVPAGSVAS-----HLGTTTSRSFYFLTATLALCLVFTV 54
 DB 1 MDPGLQALNGMAPPDGTAMHVPAGSVAS-----HLGTTTSRSFYFLTATLALCLVFTV 54

QY 55 ATIMVLVQRTSDIPNSPDNVLKGCNSEDLLCILKRAPFKKSWAYLQVAKHLNKTLS 114
 DB 60 ATIMVLVQRTSDIPNSPDNVLKGCNSEDLLCILKRAPFKKSWAYLQVAKHLNKTLS 119

QY 115 WNKDGILHGVRYQDGNLVTFQPLGYFIICQLQFLVQCPNNSVDLKLLELNKHKQALV 174
 DB 120 WNKDGILHGVRYQDGNLVTFQPLGYFIICQLQFLVQCPNNSVDLKLLELNKHKQALV 179

QY 175 TVCESGMQTKHVQNLSQFLLDYLVQNTTISVNVDTFQXIDTSTFPLENVLSTFLYSNSD 234
 DB 180 TVCESGMQTKHVQNLSQFLLDYLVQNTTISVNVDTFQXIDTSTFPLENVLSTFLYSNSD 239

RESULT 3
 FASL_MOUSE
 ID FASL_MOUSE STANDARD; PRT; 279 AA.
 AC P41047; O61217; O9R1F2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FAS ANTIGEN LIGAND.
 GN TNFSF6 OR APTILG1 OR FASL OR GLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063;
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
 Suda T., Nagata S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 mutation in the Fas ligand.";
 RL Cell 76:969-976(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;
 RX MEDLINE=95388076; PubMed=7544870;
 RA Peltsch M.J., Tschoep J.J.;
 RT "Comparative molecular modelling of the Fas-ligand and other members
 of the TNF family.";
 RL Mol. Immunol. 32:761-772(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=95196085; PubMed=7889405;
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
 TNF family gene cluster.";
 RL Immunity 1:131-136(1994).
 RN [4]

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:30:33 ; Search time 96.97 Seconds
(without alignments)
352.972 Million cell updates/sec

Title: US-09-628-126-8

Perfect score: 1220

Sequence: 1 MDPGLQQALNGMAPPGDTAM.....DTSTPLENVLSIFLYSNSD 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

```

minimum DB seq length: 0

```

```
ximum DB seq length: 2000000000
ximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

100% Processing. Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Database : SPTREMBL 17:*

```

1: sp archea:*

```

```

1: sp_bacteria:
2: sp_bacteria:*

```

```
3: sp_funqi:*
```

```
4: sp_human: *
```

```
5: sp_invertebrate:*
```

```
6: sp_mammal:*
```

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7: sp_mhc:*
```

```
8: sp_organelle:
```

```
9: sp_phage:*
```

```
10: sp_plant:*
```

```
11: sp_rodent:*
```

```
12: sp_virus:*
```

```
13: sp_vertibrate:*
```

```
14: sp_unclassified:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Query No.	Score	Match	Length	DB	ID	Description
1	1196	98.0	234	4	O43404	O43404	homo sapien
2	100	8.2	169	11	Q9WV90	Q9WV90	marimota mon
3	96.5	7.9	215	6	Q9BEE8	Q9BEE8	erinaceus e
4	95.5	7.8	280	6	Q9BDN1	Q9BDN1	cercocebus
5	94.5	7.7	234	6	Q9TJ3	Q9TJ3	equus caball
6	94	7.7	547	12	Q9B269	Q9B269	molluscum c
7	93	7.6	217	11	Q9ERG6	Q9ERG6	peromyscus
8	92	7.5	280	6	Q9MYL6	Q9MYL6	macaca neme
9	92	7.5	280	6	Q9BDM5	Q9BDM5	macaca mulla
10	89.5	7.3	892	10	Q9S9U5	Q9S9U5	arabidopsis
11	89.5	7.3	896	10	Q9M980	Q9M980	arabidopsis
12	88.5	7.3	217	6	Q9BEG1	Q9BEG1	bradypus tr
13	88	7.2	1109	5	Q9GYH7	Q9GYH7	caenorhabdi
14	87.5	7.2	216	6	Q9BEC4	Q9BEC4	taipa europ
15	87.5	7.2	813	4	Q9P4N0	Q9P4N0	homo sapien
16	87.5	7.2	1003	4	Q9P207	Q9P207	homo sapien
17	87	7.1	462	2	Q9CM44	Q9CM44	pasteurella
18	86.5	7.1	3512	5	Q62524	Q62524	chironomus
19	85	7.0	282	6	Q9BEA8	Q9BEA8	sus scrofa

ALIGNMENTS

RESULT	1
ID	O43404
AC	O43404 PRELIMINARY; PRT; 234 AA.
DT	01-JUN-1998 (TREMBlrel. 06, Created)
DT	01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE	CD30L PROTEIN.
GN	CD30L.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=98007874; PubMed=9349718;
RX	Croager E.J., Abraham L.J.;
RT	"Characterisation of the human CD30 ligand gene structure.";
RL	Biochim. Biophys. Acta 1353:231-235(1997).
DR	EWBL; AF006384; AAB97877.1; -
DR	EWBL; AF006381; AAB97877.1; JOINED.
DR	EWBL; AF006382; AAB97877.1; JOINED.
DR	EWBL; AF006383; AAB97877.1; JOINED.
DR	InterPro; IPR000478; TNF_family.
DR	InterPro; IPR003638; TNF_8.
DR	Pfam; PF00229; TNF; 1.
DR	ProDom; PD023087; TNF_8; 1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS50049; TNF_2; 1.
DR	SMART; SM00207; TNF; 1.
SQ	SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match	98.0%;	Score 1196;	DB 4;	Length 234;
Best Local Similarity	98.3%;	Pred. No. 1.5e-111;		
Matches 230;	Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;

Oy	1	MDPGLQQALNGMAPPDGTAMHVPAGSVASHLGTTTSRSFYELTATIALCLVFVATIMVL	60
Dd	1	MDPGLQQALNGMAPPDGTAMHVPAGSVASHLGTTTSRSFYELTATIALCLVFVATIMVL	60
Ov	61	VVORTDSIPNSPDNVPLKGGNCSEDLICILKRPFKKSWAYILOVAKHLNKTKLSWNKDGI	120

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|||||
Db 61 VVQRTDIPSPDNVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWKNKDI 120
QY 121 LHGVRYQDGNLVIOFPGLYFIICQLQFLVQCPNNNSVDKLELLINKHKKQALVTVCESG 180
Db 121 LHGVRYQDGNLVIOFPGLYFIICQLQFLVQCPNNNSVDKLELLINKHKKQALVTVCESG 180
QY 181 MQTKHYQNLISQFLDYLVQNTTISVNVDTFOYIDTSTFFPLENVLSIFLXNSD 234
Db 181 MQTKHYQNLISQFLDYLVQNTTISVNVDTFOYIDTSTFFPLENVLSIFLXNSD 234

RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Scurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR InterPro; IPR000478; TNF family.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;
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Query Match 8.2%; Score 100; DB 11; Length 169;
Best Local Similarity 24.6%; Pred. No. 0.03;
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;

QY 90 LKRAPFKKSWAYLQVAKHLNKTLSWKNK---GLHGVRYQDGNLVIOFPGLYFIICQLQ 146
Db 40 LRRA-----AHLTGKPNSSRSPLEWEDTYGISLSGVKYGKGLVINDTGLYFVYSKIY 93

QY 147 FLVQ-CPNNSVDKLELLINKH-----IKQALVTVCESGM-----QTKH 185
Db 94 FQSCNNQPLSHKVKYVKNSKYPODLVLMGCKMNYCTTGOMWARSSYLGVAFNFTSNDH 153

QY 186 VYQNLISQFL 195
Db 154 LYVNVSELSL 163
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RESULT 3
Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (FRAGMENT).
GN TNFA.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group.";
RL submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;
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Query Match 7.9%; Score 96.5; DB 6; Length 215;
Best Local Similarity 23.3%; Pred. No. 0.089;
Matches 47; Conservative 36; Mismatches 76; Indels 43; Gaps 10;

QY 37 SYFYLTATLALCLVFTVATIMVLVVQRTDIPSPDNVPLKGGNCSEDLCLILK--RAP 94
Db 28 SFFLVAGATTFLCLLH---FCVIGPQRDE---FPDNIQLNNA-----LAQTLRSSRTQ 74
QY 95 FKKSWAYLQVAKHLNKTLSWKNKG---ILHGVRYQDGNLVIOFPGLYFIICQLQFLVQ 150
Db 75 SDKPVAHV-VASIKSEGQLLWSEVANALLANGMKLTDNLVPLDGLYLYSQVLFGKQ 133
QY 151 -CPNNSVDKLELLINKHIK-----QALVTVCES-----GMOTKHYQNLISQF 193
Db 134 GCPSTHV-----FLTHNIKRVASVQKDVNLLSAIKSPQSETPGAEARWPYEIYL 187
QY 194 LLDYLQVNTTISVNVDTFOYID 215
Db 188 GVFOLEKGDRLSAEINLPDYLD 209
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RESULT 4
Q9BDN1 PRELIMINARY; PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CD95L PROTEIN.
GN CD95L.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostlik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344847; AAK37606.1; -.
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;
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Query Match 7.8%; Score 95.5; DB 6; Length 280;
Best Local Similarity 27.18; Pred. No. 0.15;
Matches 35; Conservative 21; Mismatches 46; Indels 27; Gaps 6;

QY 94 PFKKSW---AYLQVAKHLNKTLSWKNK-GI--LHGVRYQDGNLVIOFPGLYFIICQLQ 147
Db 137 PEKKEQRKVAHLTGKPNSSRSPLEWEDTYGIVLLSGVKYKGLVNETGLYFVYSKYVF 196
QY 148 LVQ-CPNNSVDKLELLINKH-----IKQALVTVCESGM-----QTKH 186
Db 197 RGQSCNPLSHKVKYVMNSKYPODLVLMGCKMNSYCTTGOMWAHSSYLGVAFNLTSTDL 256
QY 187 YQNLISQFL 195
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:22:25 ; Search time 39.95 Seconds
(without alignments)
131.809 Million cell updates/sec

Title: US-09-628-126-8
Perfect score: 1220
Sequence: 1 MDPGLQALNGMAPPGDTAM.....DTSTFPLENLVLSIFLYNSD 234

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Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1220	100.0	234	1 US-08-225-989-8	Sequence 8, Appli
2	1220	100.0	234	1 US-08-570-923-8	Sequence 8, Appli
3	1220	100.0	234	1 US-08-580-014-8	Sequence 8, Appli
4	1220	100.0	234	4 US-09-079-785-8	Sequence 8, Appli
5	1118	91.6	215	1 US-08-225-989-23	Sequence 23, Appli
6	1118	91.6	215	1 US-08-570-923-23	Sequence 23, Appli
7	1118	91.6	215	1 US-08-580-014-23	Sequence 23, Appli
8	1118	91.6	215	4 US-09-079-785-23	Sequence 23, Appli
9	860.5	70.5	239	1 US-08-225-989-6	Sequence 6, Appli
10	860.5	70.5	239	1 US-08-570-923-6	Sequence 6, Appli
11	860.5	70.5	239	1 US-08-580-014-6	Sequence 6, Appli
12	860.5	70.5	239	4 US-09-079-785-6	Sequence 6, Appli
13	814.5	66.8	220	1 US-08-225-989-19	Sequence 19, Appli
14	814.5	66.8	220	1 US-08-570-923-19	Sequence 19, Appli
15	814.5	66.8	220	1 US-08-580-014-19	Sequence 19, Appli
16	814.5	66.8	220	4 US-09-079-785-19	Sequence 19, Appli
17	775	63.5	148	3 US-08-584-031-12	Sequence 12, Appli
18	615	50.4	125	1 US-08-225-989-20	Sequence 20, Appli
19	615	50.4	125	1 US-08-570-923-20	Sequence 20, Appli
20	615	50.4	125	1 US-08-580-014-20	Sequence 20, Appli
21	615	50.4	125	4 US-09-079-785-20	Sequence 20, Appli
22	447.5	36.7	130	1 US-08-225-989-21	Sequence 21, Appli
23	447.5	36.7	130	1 US-08-570-923-21	Sequence 21, Appli
24	447.5	36.7	130	1 US-08-580-014-21	Sequence 21, Appli
25	447.5	36.7	130	4 US-09-079-785-21	Sequence 21, Appli
26	274	22.5	52	4 US-09-369-494-17	Sequence 17, Appli
27	274	22.5	52	4 US-09-358-569D-15	Sequence 15, Appli

28 102 8.4 279 5 PCT-US95-00362-5 Sequence 5, Appli
29 92 7.5 378 3 US-08-630-172-21 Sequence 21, Appli
30 92 7.5 378 4 US-08-375-419-21 Sequence 21, Appli
31 91.5 7.5 376 3 US-08-751-512-8 Sequence 8, Appli
32 90.5 7.4 145 3 US-08-630-172-5 Sequence 5, Appli
33 90.5 7.4 145 4 US-09-375-419-5 Sequence 5, Appli
34 90.5 7.4 179 3 US-08-649-100-9 Sequence 9, Appli
35 90.5 7.4 281 2 US-08-810-453-2 Sequence 2, Appli
36 90.5 7.4 281 3 US-08-815-190A-2 Sequence 2, Appli
37 90.5 7.4 281 4 US-09-290-640-25 Sequence 25, Appli
38 90.5 7.4 281 4 US-09-479-524-3 Sequence 3, Appli
39 90.5 7.4 281 5 PCT-US95-00362-2 Sequence 2, Appli
40 90.5 7.4 287 3 US-08-815-190A-16 Sequence 16, Appli
41 90 7.4 141 4 US-08-286-529-22 Sequence 22, Appli
42 90 7.4 149 3 US-08-584-031-17 Sequence 17, Appli
43 86 7.0 158 1 US-07-994-469A-99 Sequence 99, Appli
44 85.5 7.0 309 1 US-08-236-918A-2 Sequence 2, Appli
45 85 7.0 161 1 US-07-994-469A-61 Sequence 61, Appli

ALIGNMENTS

RESULT 1
US-08-225-989-8
; Sequence 8, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

```
;
;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 234 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-225-989-8

Query Match          100.0%; Score 1220; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 6.4e-125;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VVORTDSIPNSPDNVPLKGGNCSEDLCLILKRAPFKSWAYLOVAKHLNKTLSWKNKDI 120
QY 121 LHGVRYQDGNLVQFPGFLYFIICQLQFLVQCPNNSVDLKLKRAPFKSWAYLOVAKHLNKTLSWKNKDI 180
DB 121 LHGVRYQDGNLVQFPGFLYFIICQLQFLVQCPNNSVDLKLKRAPFKSWAYLOVAKHLNKTLSWKNKDI 180
QY 181 MQTKHVVQNLSQLLDYLDYLVQNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 234
DB 181 MQTKHVVQNLSQLLDYLDYLVQNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 234

RESULT 2
US-08-570-923-8
; Sequence 8, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 234 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-8

Query Match          100.0%; Score 1220; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 6.4e-125;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL 60
DB 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL 60
QY 61 VVORTDSIPNSPDNVPLKGGNCSEDLCLILKRAPFKSWAYLOVAKHLNKTLSWKNKDI 120
DB 61 VVORTDSIPNSPDNVPLKGGNCSEDLCLILKRAPFKSWAYLOVAKHLNKTLSWKNKDI 120
QY 121 LHGVRYQDGNLVQFPGFLYFIICQLQFLVQCPNNSVDLKLKRAPFKSWAYLOVAKHLNKTLSWKNKDI 180
DB 121 LHGVRYQDGNLVQFPGFLYFIICQLQFLVQCPNNSVDLKLKRAPFKSWAYLOVAKHLNKTLSWKNKDI 180
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RESULT 3
US-08-580-014-8
; Sequence 8, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:19:35 ; Search time 33.56 Seconds
(without alignments)
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Title: US-09-628-126-6
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Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	123	9.9	279	1	FASL_MOUSE	P41047 mus musculus
4	102	8.2	278	1	FASL_RAT	P36940 rattus norv
5	91	7.3	309	1	41BL_MOUSE	P41274 mus musculus
6	89.5	7.2	235	1	TNFA_PERLE	P36939 peromyscus
7	87	7.0	281	1	FASL_HUMAN	P48023 homo sapien
8	86.5	6.9	233	1	TNFA_MACMU	P48094 macaca mula
9	85	6.9	2194	1	SC16_YEAST	P48415 saccharomyc
10	85	6.8	291	1	TN10_MOUSE	P50592 mus musculus
11	84.5	6.8	525	1	C307_DROME	Q9vrm7 drosophila
12	83.5	6.7	201	1	TNFB_MACEU	Q9xt48 macropus eu
13	83.5	6.7	233	1	TNFA_MACEU	P79337 macaca fasc
14	82.5	6.6	233	1	TNFA_PAPHU	O77510 papio hamad
15	82.5	6.6	965	1	AMPN_MOUSE	P97449 mus musculus
16	82.5	6.6	1078	1	S24A_HUMAN	O95486 homo sapien
17	82	6.6	234	1	TNFA_SHEEP	P23383 ovis aries
18	81.5	6.5	233	1	TNFA_CANEA	P51742 canis faml
19	81	6.5	460	1	ENV_HV123	P12491 human immun
20	80.5	6.5	1376	1	RPOD_ARATH	P56764 arabidopsis
21	79.5	6.4	383	1	COS7_YEAST	Q07788 saccharomyc
22	79	6.3	229	1	TNFA_CEREL	P51743 cervus elap
23	79	6.3	851	1	NUD1_YEAST	P32336 saccharomyc
24	78.5	6.3	234	1	TNFA_HORSE	P29553 equus cabal
25	78.5	6.3	235	1	TNFA_RAT	P16599 rattus norv
26	78.5	6.3	507	1	C392_DROME	P82713 drosophila
27	78.5	6.3	815	1	NEL2_RAT	Q62918 rattus norv
28	78.5	6.3	1150	1	IRR1_YEAST	P40541 saccharomyc
29	78	6.3	396	1	BMP2_HUMAN	P12643 homo sapien
30	78	6.3	856	1	ENV_HV1MN	P05877 human immun
31	77.5	6.2	178	1	IL10_MACFA	P79338 macaca fasc
32	77.5	6.2	463	1	YRN3_YEAST	P36066 saccharomyc
33	77.5	6.2	1583	1	MIS4_SCHPO	Q09725 schizosacch

ALIGNMENTS

RESULT 1
TNFB_MOUSE STANDARD; PRT; 239 AA.
ID TNFB_MOUSE
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=T-cell;
RC MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
BA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
ligand defines an emerging family of cytokines with homology to
TNF".
RT Cell 73:1349-1360(1993).
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL; L09754; AAA74595.1; -.
DR PIR; B40710; B40710.
DR MGD; MGI:88328; Tnfsf8.
DR InterPro; IPR003638; TNF_8.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD023087; TNF_8; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PSS00049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
KW Cytoplasmic (POTENTIAL).
FT DOMAIN 1 43
FT TRANSMEM 44 67
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 68 239
FT CARBOHYD 75 75
FT CARBOHYD 86 86
FT CARBOHYD 114 114
FT CARBOHYD 158 158
FT CARBOHYD 158 158

34 77 6.2 795 1 SYFB_BUCAI P57230 buchnera ap
35 76.5 6.1 317 1 TN11_HUMAN O14788 h tumor nec
36 76.5 6.1 345 1 OPCM_BOVIN P11834 bos taurus
37 76.5 6.1 1073 1 HSER_PIG P5204 sus scrofa
38 76 6.1 234 1 TNFA_CAVPO Q9v557 cavia porce
39 76 6.1 520 1 C4P2_DROME Q9v557 cavia porce
40 75.5 6.1 178 1 IL10_CERTO P46651 cercocebus
41 75.5 6.1 383 1 COS5_YEAST P47187 saccharomyc
42 75.5 6.1 1178 1 PH81_YEAST P17442 saccharomyc
43 75 6.0 179 1 I10H_HSV2 Q89451 equine herp
44 75 6.0 524 1 2A5G_HUMAN Q13362 h serine/th
45 75 6.0 524 1 2A5G_RABIT Q28651 o serine/th

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FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.1e-107;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 60
DQ 1 MEPLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 60
QY 61 IILVIVVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSW 120
DQ 61 IILVIVVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSW 120
QY 121 NEDGTHGLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLV 180
DQ 121 NEDGTHGLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLV 180
QY 181 VCESGVQSKNIYQNLQSLFLLHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 239
DQ 181 VCESGVQSKNIYQNLQSLFLLHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 239

RESULT 2
TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971.
DT 01-OCT-1993 (Rel. 27, Created).
DT 01-OCT-1993 (Rel. 27, Last sequence update).
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93313964; PubMed=8301931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RA "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RA ligand defines an emerging family of cytokines with homology to
RA TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry.
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L09753; AAA74594.1;
DR PIR; A40710; A40710.
DR MIM; 603875;
DR InterPro; IPR003638; TNF.8.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD023087; TNF.8; 1.
DR SMART; SM00207; TNF; 1.
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DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 37
FT TRANSMEM 38 62
FT DOMAIN 63 234
FT CARBOHYD 81 81
FT CARBOHYD 109 109
FT CARBOHYD 153 153
FT CARBOHYD 189 189
FT CARBOHYD 201 201
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 69.1%; Score 860.5; DB 1; Length 234;
Best Local Similarity 69.6%; Pred. No. 8.6e-72;
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

QY 1 MEPLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 59
DQ 1 MDPLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 54
QY 60 AILVIVVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLS 119
DQ 55 AILVIVVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLS 114
QY 120 WNEDGTHGLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLV 179
DQ 115 WNKDGLHGVRYQDGNLIVQFPGLYFIVCQLQFLVQCPNNSVDLKLLELHKKQALV 174
QY 180 TVCESGVQSKNIYQNLQSLFLLHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 239
DQ 175 TVCESGMQTHVYQNLQSLFLLHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 234

RESULT 3
FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTL1G1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RA "Generalized lymphoproliferative disease in mice, caused by a point
RA mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschoep J.J.;
RA "Comparative molecular modelling of the Fas-ligand and other members
RA of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RA "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RA TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:17:50 ; Search time 96.97 Seconds
(without alignments)
360.514 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNFPDLNVLSVFLYSSSD 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : *SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	840.5	67.5	234	043404	Q43404 homo sapien
2	90.5	7.3	797	12 Q99BY2	Q99BY2 human immun
3	90	7.2	280	6 Q9WY16	Q9WY16 macaca neme
4	89.5	7.2	225	13 Q9IB42	Q9IB42 paralichthy
5	89.5	7.2	401	2 P72902	P72902 synechocyst
6	89.5	7.2	847	12 Q9WIS1	Q9WIS1 human immun
7	89	7.1	169	11 Q9WV90	Q9WV90 marmota mon
8	88	7.1	234	6 Q28320	Q28320 capra hircu
9	87.5	7.0	896	10 Q9M9H0	Q9M9H0 arabadopsi
10	87	7.0	858	12 Q99C07	Q99C07 human immun
11	87	7.0	2013	5 Q96216	Q96216 plasmodium
12	86.5	6.9	217	11 Q9ERG6	Q9ERG6 peromyscus
13	86.5	6.9	280	6 Q9BDN1	Q9BDN1 cercocobus
14	86.5	6.9	280	6 Q9BDM5	Q9BDM5 macaca mula
15	86.5	6.9	579	4 Q9BY79	Q9BY79 homo sapien
16	86.5	6.9	2195	3 Q02822	Q02822 saccharomyc
17	86	6.9	674	3 Q06629	Q06629 saccharomyc
18	85.5	6.9	282	6 Q9BEA8	Q9BEA8 sus scrofa
19	85.5	6.9	873	10 Q9FID8	Q9FID8 arabadopsi

Q9C637 arabadopsi
Q9FKU2 arabadopsi
Q9DPZ6 human immun
Q99BZ7 human immun
Q68241 pantoaea cit
Q81069 arabadopsi
Q9IC83 kaposi's sa
Q9DC72 mus musculu
Q98ST8 brachydanio
Q64940 avian infec
Q9SDA5 arabadopsi
Q9SNA3 arabadopsi
Q9XK63 mus musculu
Q9POV5 homo sapien
Q9T0J1 arabadopsi
Q9P20 globodera r
Q94382 caenorhabdi
Q94383 caenorhabdi
Q9K5C7 claviabacter
Q9SUN4 arabadopsi
Q9LQ11 arabadopsi
Q9DPR7 meleagrid h
Q9ELH3 meleagrid h
Q9BEC4 talpa europ
Q81781 arabadopsi
Q9FX99 arabadopsi

ALIGNMENTS

RESULT 1
O43404 PRELIMINARY; PRT; 234 AA.
AC O43404;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD30L PROTEIN.
GN CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007874; PubMed=9349718;
RA Croager E.J., Abraham L.J.;
RT "Characterisation of the human CD30 ligand gene structure.";
RL Biochim. Biophys. Acta 1353:231-235(1997).
DR EMBL; AF006384; AAB97877.1;
DR EMBL; AF006381; AAB97877.1; JOINED.
DR EMBL; AF006382; AAB97877.1; JOINED.
DR EMBL; AF006383; AAB97877.1; JOINED.
DR InterPro; IPR000478; TNF family.
DR InterPro; IPR003638; TNF_8.
DR Pfam; PF00229; TNF_1.
DR ProDom; PD023087; TNF_8; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 67.5%; Score 840.5; DB 4; Length 234;
Best Local Similarity 68.3%; Pred. No. 3.4e-72;
Matches 164; Conservative 28; Mismatches 41; Indels 7; Gaps 2;

QY 1 MEPLQAGSCGAPSPDPAMQVQPGSVASPRWRTRPWRSTSRSFYLSTTAL-VCLVAV 59
Db 1 MDPGLQALNGMAPPGDTAMHVPAGSVAS-----HLGTTSRSFYLTATLALCLVFTV 54
QY 60 AIIIVLVQVKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLS 119

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:16:15 ; Search time 39.95 Seconds
(without alignments)
134.625 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNFTPLDNLVFLYSSD 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1246	100.0	239	1	US-08-225-989-6 Sequence 6, Appli
2	1246	100.0	239	1	US-08-570-923-6 Sequence 6, Appli
3	1246	100.0	239	1	US-08-580-014-6 Sequence 6, Appli
4	1246	100.0	239	4	US-09-079-785-6 Sequence 6, Appli
5	1141	91.6	220	1	US-08-225-989-19 Sequence 19, Appl
6	1141	91.6	220	1	US-08-570-923-19 Sequence 19, Appl
7	1141	91.6	220	1	US-08-580-014-19 Sequence 19, Appl
8	1141	91.6	220	4	US-09-079-785-19 Sequence 19, Appl
9	860.5	69.1	234	1	US-08-225-989-8 Sequence 8, Appli
10	860.5	69.1	234	1	US-08-570-923-8 Sequence 8, Appli
11	860.5	69.1	234	1	US-08-580-014-8 Sequence 8, Appli
12	860.5	69.1	234	4	US-09-079-785-8 Sequence 8, Appli
13	814.5	65.4	215	1	US-08-225-989-23 Sequence 23, Appl
14	814.5	65.4	215	1	US-08-570-923-23 Sequence 23, Appl
15	814.5	65.4	215	1	US-08-580-014-23 Sequence 23, Appl
16	814.5	65.4	215	4	US-09-079-785-23 Sequence 23, Appl
17	685	55.0	130	1	US-08-225-989-21 Sequence 21, Appl
18	685	55.0	130	1	US-08-570-923-21 Sequence 21, Appl
19	685	55.0	130	1	US-08-580-014-21 Sequence 21, Appl
20	685	55.0	130	4	US-09-079-785-21 Sequence 21, Appl
21	624	50.1	148	3	US-08-584-031-12 Sequence 12, Appl
22	391.5	31.4	125	1	US-08-225-989-20 Sequence 20, Appl
23	391.5	31.4	125	1	US-08-570-923-20 Sequence 20, Appl
24	391.5	31.4	125	1	US-08-580-014-20 Sequence 20, Appl
25	391.5	31.4	125	4	US-09-079-785-20 Sequence 20, Appl
26	229	18.4	52	4	US-09-369-494-17 Sequence 17, Appl
27	229	18.4	52	4	US-09-358-569D-15 Sequence 15, Appl

28 115 9.2 279 5 PCT-US95-00362-5 Sequence 5, Appli
29 91 7.3 309 1 US-08-236-918A-2 Sequence 2, Appli
30 87 7.0 281 2 US-08-810-453-2 Sequence 2, Appli
31 87 7.0 281 3 US-08-815-190A-2 Sequence 2, Appli
32 87 7.0 281 4 US-09-290-640-25 Sequence 25, Appli
33 87 7.0 281 4 US-09-479-524-3 Sequence 3, Appli
34 87 7.0 281 5 PCT-US95-00362-2 Sequence 2, Appli
35 85 6.8 291 1 US-08-670-354-6 Sequence 6, Appli
36 85 6.8 291 4 US-09-320-424-6 Sequence 6, Appli
37 85 6.8 291 5 PCT-US96-10895-6 Sequence 6, Appli
38 83 5 6.7 287 3 US-08-815-190A-16 Sequence 16, Appli
39 83 6.7 550 2 US-08-417-210A-140 Sequence 140, App
40 83 6.7 551 2 US-08-417-210A-137 Sequence 137, App
41 83 6.7 551 2 US-08-417-210A-143 Sequence 143, App
42 83 6.7 857 1 US-08-022-835-4 Sequence 4, Appli
43 83 6.7 857 1 US-08-388-809-4 Sequence 4, Appli
44 83 6.7 857 2 US-08-647-714-4 Sequence 4, Appli
45 82.5 6.6 183 4 US-09-105-343A-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-225-989-6
; Sequence 6, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

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;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-225-989-6

Query Match          100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.3e-116;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGLOQAGSCGAPSPDPAMQVPGSVASPRWSTRSFYLTALVCLVAVVA 60
DB 1 MEGLOQAGSCGAPSPDPAMQVPGSVASPRWSTRSFYLTALVCLVAVVA 60
QY 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
DB 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
QY 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
DB 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
QY 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239
DB 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239

* RESULT 2
US-08-570-923-6
; Sequence 6, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-6

Query Match          100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.3e-116;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGLOQAGSCGAPSPDPAMQVPGSVASPRWSTRSFYLTALVCLVAVVA 60
DB 1 MEGLOQAGSCGAPSPDPAMQVPGSVASPRWSTRSFYLTALVCLVAVVA 60
QY 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
DB 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
QY 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
DB 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
QY 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239
DB 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239

RESULT 3
US-08-580-014-6
; Sequence 6, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:17:45 ; Search time 55.1 Seconds
(Without alignments)
304.145 Million cell updates/sec

Title: US-09-628-126-19
Perfect score: 1141
Sequence: 1 MQVPGSVASPRSTRPWS.....DTNTFPLDNLVSLFLSSD 220
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

imum DB seq length: 0
imum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	100.0	239	2 B40710	CD30 ligand - mous
2	814.5	71.4	234	2 A40710	CD30 ligand - huma
3	109	9.6	279	2 A53062	Fas ligand - mouse
4	91	8.0	278	2 A49266	fas ligand - rat
5	89.5	7.8	401	2 S74767	hypothetical prote
6	88.5	7.8	309	2 I53384	4-1BB ligand - mou
7	87.5	7.7	235	2 I54490	tumor necrosis fac
8	87	7.6	2013	2 C71610	probable membrane
9	86.5	7.6	2195	2 S61103	SEC16 protein - ye
10	86	7.5	674	2 S61181	hypothetical prote
11	85.5	7.5	994	2 H96510	probable disease r
12	84.5	7.4	884	2 T02731	serine/threonine-s
13	84	7.4	281	2 I38707	Fas ligand - human
14	84	7.4	1110	2 F84547	probable disease r
15	82	7.2	234	1 JH0529	tumor necrosis fac
16	81.5	7.1	304	2 T27593	hypothetical prote
17	81.5	7.1	304	2 T27594	hypothetical prote
18	81	7.1	866	2 T10587	serine/threonine-s
19	80.5	7.1	344	2 T05104	hypothetical prote
20	80	7.0	165	2 H64460	hypothetical prote
21	80	7.0	369	2 S77028	protein kinase, 41
22	79.5	7.0	889	2 T45691	receptor-like prot
23	79	6.9	851	2 S67285	NUD1 protein - ya
24	78.5	6.9	234	1 J01344	tumor necrosis fac
25	78.5	6.9	235	2 JH0029	tumor necrosis fac
26	78.5	6.9	1150	2 S49956	probable membrane
27	78	6.8	427	2 T40064	hypothetical prote
28	78	6.8	616	2 T32131	hypothetical prote
29	78	6.8	859	1 VCLJMN	env polypeptide pr

30	77.5	6.8	463	2 S37962	probable purine nu
31	77.5	6.8	1583	2 S59644	sister chromatid c
32	77	6.7	428	2 T48284	hypothetical prote
33	77	6.7	568	2 T20421	hypothetical prote
34	77	6.7	769	2 T39089	hypothetical prote
35	77	6.7	795	2 H84944	phenylalanine--trN
36	76.5	6.7	345	2 S03199	opioid-binding pro
37	76.5	6.7	1083	2 A38919	hypothetical prote
38	76.5	6.7	1223	2 T17345	hypothetical prote
39	76	6.7	205	2 H71639	NADH dehydrogenase
40	76	6.7	665	2 T06082	protein kinase hom
41	76	6.7	1313	2 G82887	hypothetical prote
42	75.5	6.6	208	2 B86877	ABC transporter AT
43	75.5	6.6	251	2 T25121	hypothetical prote
44	75.5	6.6	303	2 T25114	hypothetical prote
45	75.5	6.6	659	2 T49277	hypothetical prote

ALIGNMENTS

RESULT 1
B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, R.; Smith, C.A.; Galk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Alderson, M.; Falk, B.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, R.; Smith, C.A.; Galk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <SMI>
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match	100.0%;	Score 1141;	DB 2;	Length 239;
Best Local Similarity	100.0%;	Pred. No. 1.8e-96;		
Matches 220;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQVPGSVASPRSTRPWSRSTSRYSFYLTALVCLVAVAIILVTVVQKXKDSPTNTTEK	60	
Db	20	MQVPGSVASPRSTRPWSRSTSRYSFYLTALVCLVAVAIILVTVVQKXKDSPTNTTEK	79	
QY	61	APLKGNCSEDLFCTLKSTPKSKSWAYLQVSKHLNNTKLSWATCT.HGLIYQDGNLIVQ	120	
Db	80	APLKGNCSEDLFCTLKSTPKSKSWAYLQVSKHLNNTKLSWEDGTIHLIYQDGNLIVQ	139	
QY	121	FPGLYFTVCOQLVQCSNHSVDLTQLLLINSKIKKOTLVTVCSGVOSKNIIYQNLSOFL	180	
Db	140	FPGLYFTVCOQLVQCSNHSVDLTQLLLINSKIKKOTLVTVCSGVOSKNIIYQNLSOFL	199	
QY	181	LHYLVQNVSTISVRVDNFQYVDNTFPLDNLVSLFLSSD	220	
Db	200	LHYLVQNVSTISVRVDNFQYVDNTFPLDNLVSLFLSSD	239	

RESULT 2
A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, R.; Smith, C.A.; Galk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Alderson, M.; Falk, B.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, R.; Smith, C.A.; Galk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:31:35 ; Search time 33.56 Seconds
(without alignments)
240.353 Million cell updates/sec

Title: US-09-628-126-19

Perfect score: 1141

Sequence: 1 MQVPGSVASPWSTRPWRS.....DTNFTPLDNLVSLFLYSSSD 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1141	100.0	239	1 TNF8_MOUSE	P32972 mus musculus
2	814.5	71.4	234	1 TNF8_HUMAN	P32971 homo sapien
3	109	9.6	279	1 FASL_MOUSE	P41047 mus musculus
4	91	8.0	278	1 FASL_RAT	P36940 rattus norv
5	88.5	7.8	309	1 41BL_MOUSE	P41274 mus musculus
6	87.5	7.7	235	1 TNFA_PERLE	P36939 peromyscus
7	86.5	7.6	2194	1 SC16_YEAST	P48415 saccharomyc
8	85	7.4	291	1 TN10_MOUSE	P50592 mus musculus
9	84.5	7.4	233	1 TNFA_MACMU	P48094 macaca mula
10	84.5	7.4	525	1 C307_DROME	Q9vrm7 drosophila
11	84	7.4	281	1 FASL_HUMAN	P48023 homo sapien
12	83.5	7.3	201	1 TNFB_WACEU	Q9xt48 macropus eu
13	82.5	7.2	965	1 TNFA_MOUSE	P97449 mus musculus
14	82	7.2	234	1 TNFA_SHEEP	P23383 ovis aries
15	81.5	7.1	233	1 TNFA_CANFA	P51742 canis famil
16	81.5	7.1	233	1 TNFA_MACFA	P79337 macaca fasc
17	81	7.1	460	1 ENV_HV123	P12491 human immun
18	80.5	7.1	233	1 TNFA_FAPHU	O77510 papio hamad
19	80	7.0	1376	1 RPOD_ARATH	P56764 arabidopsis
20	79	6.9	229	1 TNFA_CEREL	P51743 cervus elap
21	79	6.9	851	1 NUD1_YEAST	P23236 saccharomyc
22	78.5	6.9	234	1 TNFA_HORSE	P29553 equus cabal
23	78.5	6.9	235	1 TNFA_RAT	P16599 rattus norv
24	78.5	6.9	1150	1 IRR1_YEAST	P40541 saccharomyc
25	78	6.8	856	1 ENV_HVIMN	P05877 human immun
26	77.5	6.8	178	1 IL10_MACFA	P79338 macaca fasc
27	77.5	6.8	463	1 YK3_YEAST	P36066 saccharomyc
28	77.5	6.8	1583	1 MISA_SCHPO	Q09725 schizosacch
29	77	6.7	795	1 SYFB_BUCAI	P57230 buchnera ap
30	76.5	6.7	317	1 TN11_HUMAN	O14788 h tumor nec
31	76.5	6.7	345	1 OPCM_BOVIN	P11834 bos taurus
32	76.5	6.7	507	1 C392_DROME	P82713 drosophila
33	76.5	6.7	1073	1 HSER_PIG	P55204 sus scrofa

ALIGNMENTS

RESULT 1

ID	TNF8_MOUSE	STANDARD;	PRT;	239 AA.
AC	P32972;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	CD30 LIGAND (CD30-L).			
GN	TNFSF8 OR CD30LG OR CD30L.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=T-cell;			
RC	MEDLINE=3313964; PubMed=8391931;			
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,			
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,			
RA	Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,			
RA	Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.,			
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose			
RT	ligand defines an emerging family of cytokines with homology to			
RT	TNF."			
RL	Cell 73:1349-1360(1993).			
CC	-1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF			
CC	T CELLS.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (CC			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: L09754; AAA74595.1; ..			
DR	PIR: B40710; B40710.			
DR	MGI: 88328; Tnfsf8.			
DR	InterPro: IPR003638; TNF_8.			
DR	InterPro: IPR000478; TNF_family.			
DR	Pfam: PF00229; TNF; 1.			
DR	ProDom: PD023087; TNF_8; 1.			
DR	SMART: SM00207; TNF; 1.			
DR	PROSITE: PS00251; TNF_1; 1.			
DR	PROSITE: PS50049; TNF_2; 1.			
DR	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.			
FT	DOMAIN 1 43			
FT	TRANSMEM 44 67			
FT	DOMAIN 68 239			
FT	CARBOHYD 75 75			
FT	CARBOHYD 86 86			
FT	CARBOHYD 114 114			
FT	CARBOHYD 158 158			
FT	CARBOHYD 158 158			

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FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 100.0%; Score 1141; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e-97;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQVQPGSVASPRSTRPWRSTSRYSFYLSSTALVCLVAVAIILVVQVKDSTPNTTEK 60
Db 20 MQVQPGSVASPRSTRPWRSTSRYSFYLSSTALVCLVAVAIILVVQVKDSTPNTTEK 79

Qy 61 APLKGGNCSEDLFTLKSTPSKSWAYLVQSKHLNNTKLSWNEDGTHGLIYQDGNLIVQ 120
Db 80 APLKGGNCSEDLFTLKSTPSKSWAYLVQSKHLNNTKLSWNEDGTHGLIYQDGNLIVQ 139

Qy 121 FPGLYFYVICOQLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 180
Db 140 FPGLYFYVICOQLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 199

Qy 181 LHYLVQNSTISVRVDFNQYVDNTFPLDNVLSVFLYSSSD 220
Db 200 LHYLVQNSTISVRVDFNQYVDNTFPLDNVLSVFLYSSSD 239

RESULT 2
TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
-GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Arnitage R.J.;
RA "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF.";
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOME=CD guide CD153 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; L09753; AAA74594.1; -.
CC PIR; A40710; A40710.
CC MIM; 603875;
CC InterPro; IPR003638; TNF_8.
CC InterPro; IPR000478; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD023087; TNF_8; 1.
CC SMART; SM00207; TNF; 1.
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DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 63 234 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1b CRC64;

Query Match 71.4%; Score 814.5; DB 1; Length 234;
Best Local Similarity 70.6%; Pred. No. 2.7e-67;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQPGSVASPRSTRPWRSTSRYSFYLSSTALVCLVAVAIILVVQVKDSTPNTTE 59
Db 20 MHVPAGSVAS-----HLGTTSRYSFYLTATLALCLVFTVAFIMVLVQVQRTDSINSPD 73

Qy 60 KAPLKGNCSEDLFTLKSTPSKSWAYLVQSKHLNNTKLSWNEDGTHGLIYQDGNLIV 119
Db 74 NVPLKGGNCSEDLFTLKSTPSKSWAYLVQSKHLNNTKLSWNEDGTHGLIYQDGNLIV 133

Qy 120 QPGLFYVICOQLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 179
Db 134 QPGLFYVICOQLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 193

Qy 180 LHYLVQNSTISVRVDFNQYVDNTFPLDNVLSVFLYSSSD 220
Db 194 LLDYLVQNSTISVRVDFNQYVDNTFPLDNVLSVFLYSSSD 234

RESULT 3
FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLGI OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
[2]
SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RX STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peltsch M.J., Tschoep J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
[3]
SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
[4]
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2002, 08:30:35 ; Search time 96.97 Seconds
(without alignments)
331.854 Million cell updates/sec

Title: US-09-628-126-19
Perfect score: 1141
Sequence: 1 MQVPGSVASVWSPRSTRPWS.....DTNTFPLDNVLSVFLYSSD 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	794.5	69.6	234	043404	Q43404 homo sapien
2	90.5	7.9	797	12 Q99BY2	Q99by2 human immun
3	89.5	7.8	225	13 Q9IB42	Q9ib42 paralichthy
4	89.5	7.8	401	2 PZ2902	PZ2902 synechocyst
5	89.5	7.8	847	12 Q9WIS1	Q9wis1 human immun
6	89	7.8	169	11 Q9WV90	Q9wv90 marmota mon
7	88	7.7	234	6 Q28320	Q28320 capra hircu
8	87	7.6	858	12 Q99C07	Q99c07 human immun
9	87	7.6	896	10 Q9M9B0	Q9m9b0 arabidopsis
10	87	7.6	2013	5 Q96216	Q96216 plasmodium
11	86.5	7.6	2195	3 Q92822	Q92822 saccharomyc
12	86	7.5	280	6 Q9MYL6	Q9myl6 macaca neme
13	86	7.5	280	6 Q9BDN1	Q9bdn1 cercocobus
14	86	7.5	280	6 Q9BDM5	Q9bdm5 macaca mula
15	86	7.5	674	3 Q06629	Q06629 saccharomyc
16	85.5	7.5	994	10 Q9C637	Q9c637 arabidopsis
17	85	7.4	699	12 Q9DPZ6	Q9dpz6 human immun
18	85	7.4	852	12 Q99BZ7	Q99bz7 human immun
19	84.5	7.4	208	2 Q68241	Q68241 pantoea cit

20	84.5	7.4	217	11 Q9ERG6	Q9erg6 peromyscus
21	84.5	7.4	884	10 Q81069	Q81069 arabidopsis
22	84	7.4	424	11 Q9DC72	Q9dc72 mus musculu
23	84	7.4	1110	10 Q9SDA5	Q9sda5 arabidopsis
24	83	7.3	282	6 Q9BEA8	Q9bea8 sus scrofa
25	82.5	7.2	966	11 Q99K63	Q99k63 mus musculu
26	82	7.2	282	12 Q9IC83	Q9ic83 kaposi's sa
27	81.5	7.1	151	5 Q9GP20	Q9gp20 globodera r
28	81.5	7.1	304	5 Q94382	Q94382 caenorhabdi
29	81.5	7.1	304	5 Q94383	Q94383 caenorhabdi
30	81	7.1	866	10 Q9SUN4	Q9sun4 arabidopsis
31	81	7.1	1391	12 Q9DPR7	Q9dpr7 meleagrid h
32	81	7.1	1409	12 Q9ELH3	Q9elh3 meleagrid h
33	80.5	7.1	216	6 Q9BEC4	Q9bec4 talpa europ
34	80.5	7.1	344	10 Q81781	Q81781 arabidopsis
35	80	7.0	165	1 Q58685	Q58685 methanococc
36	80	7.0	232	4 Q9UIV3	Q9uiv3 homo sapien
37	80	7.0	358	12 Q71050	Q71050 human immun
38	80	7.0	369	2 Q55952	Q55952 synechocyst
39	80	7.0	400	12 Q11578	Q11578 human immun
40	80	7.0	403	12 Q11580	Q11580 human immun
41	79.5	7.0	399	12 Q11584	Q11584 human immun
42	79.5	7.0	889	10 Q9SNA3	Q9sna3 arabidopsis
43	79	6.9	350	4 Q9NSP7	Q9nsp7 homo sapien
44	79	6.9	364	4 Q9HB11	Q9hb11 homo sapien
45	79	6.9	366	2 Q9REN2	Q9ren2 buchnera ap

ALIGNMENTS

RESULT 1
ID Q43404 PRELIMINARY; PRT; 234 AA.
AC Q43404;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD30L PROTEIN.
GN CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007874; PubMed=9349718;
RA Croager E.J., Abraham L.J.;
RT "Characterisation of the human CD30 ligand gene structure.";
RL Biochim. Biophys. Acta 1353:231-235(1997).
DR EMBL; AF006384; AAB97877.1;
DR EMBL; AF006381; AAB97877.1; JOINED.
DR EMBL; AF006382; AAB97877.1; JOINED.
DR EMBL; AF006383; AAB97877.1; JOINED.
DR InterPro; IPR000478; TNF_family.
DR InterPro; IPR003638; TNF_8.
DR Pfam; PF002229; TNF; 1.
DR PRODOM; PD023087; TNF_8; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 69.6%; Score 794.5; DB 4; Length 234;
Best Local Similarity 69.2%; Pred. No. 2.3e-68;
Matches 153; Conservative 26; Mismatches 35; Indels 7; Gaps 2;

QY 1 MQVPGSVASVWSPRSTRPWSRSTFYFLSTAL-VCLVVAAILLVVQVKDSTPNTTE 59
+ + + + + : + + + + + : + + + + + : + + + + + : + + + + + :
Db 20 MHPVAGSVAS-----HLGTTSRSYFLTTATLALCLVFTVATIMLVVQRTDSIPNSPD 73
QY 60 KAPLKGNCSEDLFLCTLKTSTPSKKSWAYLQYSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119

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Db 74 NVPLKGCNCSDDLCLIKRAPFKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVI 133
QY 120 OFFGLYFIVCOLQFLVQCSNHSVDLTQLLLINSIKKQTLVTVCGESGVQSKNIYQNLISQF 179
Db 134 OFFGLYFIIQQLQFLVQCPNNSVDLKKXELLINKHKQXLVTVCGESGMQTKHVYQNLISQF 193
QY 180 LLHYLQVNSTISVRVDFNQVDFNTFFDLNVLVSFLSSSD 220
Db 194 LLDYLVQNTTISVNDVTXQIDTSTFFLENVLSIFLXNSD 234

RESULT 2
QY99BY2 PRELIMINARY; PRT; 797 AA.
ID Q99BY2;
AC Q99BY2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Suthent R., Srisurapanon S.;
RT "Biological and immunological characteristics of HIV-1 subtype E in cerebrospinal fluid and blood.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322200; AAK09407.1; -
FT NON_TER 797
FT SEQUENCE 797 AA; 90476 MW; 1C192A1DE05992C2 CRC64;

Query Match 7.9%; Score 90.5; DB 12; Length 797;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 43; Conservative 36; Mismatches 59; Indels 53; Gaps 11;

QY 40 VAILLVVQKDKSTPNTTEKAPLKGNCSEDL-FCTLKST---PSKKSWAY-----LQV 90
Db 72 LCVTLEKTEAKLNKTTNTND-PKIGNLTDEVNRCSFKMTTELKDKKQKVYALFYKLDI 130
QY 91 SKHLNNTKLSWEDGTIHLGIYODGNLIVO-----FPGLYFIV----- 128
Db 131 VPKEKNNSYSE-----YRLNCTSVIRQACPKISFDPIPIHYCTPAGTAYILKCNCKNF 186
QY 129 -----COLQFLVQCSNHSVD--LTQLLLINSIKKQTLVTVCGESGVQSKNIYQNLISQFLL 181
Db 187 NGTGPCKNVSSVQCT-HGIKPVVTTQLLNGSLAEERII-----IRSENLTNNAKNIIV 239
QY 182 HY---LQVNST 189
Db 240 HLKNSVEINCT 250

RESULT 3
QY9IB42 PRELIMINARY; PRT; 225 AA.
ID Q9IB42;
AC Q9IB42;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidel; Bothidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
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RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis factor (TNF) cDNA and gene from Japanese flounder Paralicthys olivaceus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040448; BAA94969.1; -
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNCRSISFCT.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 7.8%; Score 89.5; DB 13; Length 225;
Best Local Similarity 25.4%; Pred. No. 0.7;
Matches 31; Conservative 23; Mismatches 57; Indels 11; Gaps 5;

QY 33 LVCLVVAVAILLVVQKDKSTPNTTEKAPLKGNCSE--DLFCTLKSTPSK-KSWAYL- 88
Db 10 IVALCLGVLAFSWYTNKSEMMTQSGQTAAALSKQDKAEKTEPHNTLRQISSRAKAHLE 69
QY 89 ---QVSKHLNNTKLSW-NEDG---TIHGLIYODGNLIVPGLYFIVCOLQFLVQCSNHS 141
Db 70 GRDEEETSENKLVKNDEGLAFTQGGPELVNDHIIIPRSGLYFVYSQASFRVSCSDD 129
QY 142 VD 143
Db 130 AD 131

RESULT 4
ID P72902 PRELIMINARY; PRT; 401 AA.
AC P72902;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN.
GN SUR1066.
OS Synecochystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecochystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synecochystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90901; BAA16918.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 401 AA; 45951 MW; 9A8C3E0C64933271 CRC64;

Query Match 7.8%; Score 89.5; DB 2; Length 401;
Best Local Similarity 26.6%; Pred. No. 1.3;
Matches 42; Conservative 13; Mismatches 50; Indels 53; Gaps 6;

QY 71 DLFCTLKSTPSKKSWAYL-----QVSKHLN-----NTKLSWNEGDGTH 108
Db 47 DAFPEIKSLPKLLWLRLFWPSPSQRAKEYIQKHANFFDIIDAQOQGNLPFSKEE----- 101
QY 109 GLIYQDGNLIVQFPGLYFIVCOLQFLVQ-----CSNHSVDLTQLLLINSIKKQTLVTV 162
Db 102 --LAFNGTLLIVRSVGLYAFHQFQELVQKTNLSGNVNNVFKLLLRKLRKIKQKQN---- 155
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:22:26 ; Search time 39.95 Seconds
(without alignments)
123.923 Million cell updates/sec

Title: US-09-628-126-19
Perfect score: 1141
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Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2.6/ptodata/2/1aa/6A-COMB.pep.*
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5: /cgn2.6/ptodata/2/1aa/PCTUS-COMB.pep.*
6: /cgn2.6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match	Length	DB ID	Description
	Score	%				
1	1141	100.0	220	1	US-08-225-989-19	Sequence 19, Appl
2	1141	100.0	220	1	US-08-570-923-19	Sequence 19, Appl
3	1141	100.0	220	1	US-08-580-014-19	Sequence 19, Appl
4	1141	100.0	220	4	US-09-079-785-19	Sequence 19, Appl
5	1141	100.0	239	1	US-08-225-989-6	Sequence 6, Appl
6	1141	100.0	239	1	US-08-570-923-6	Sequence 6, Appl
7	1141	100.0	239	1	US-08-580-014-6	Sequence 6, Appl
8	1141	100.0	239	4	US-09-079-785-6	Sequence 6, Appl
9	814.5	71.4	215	1	US-08-225-989-23	Sequence 23, Appl
10	814.5	71.4	215	1	US-08-570-923-23	Sequence 23, Appl
11	814.5	71.4	215	1	US-08-580-014-23	Sequence 23, Appl
12	814.5	71.4	215	4	US-09-079-785-23	Sequence 23, Appl
13	814.5	71.4	234	1	US-08-225-989-8	Sequence 8, Appl
14	814.5	71.4	234	1	US-08-570-923-8	Sequence 8, Appl
15	814.5	71.4	234	1	US-08-580-014-8	Sequence 8, Appl
16	814.5	71.4	234	4	US-09-079-785-8	Sequence 8, Appl
17	685	60.0	130	1	US-08-225-989-21	Sequence 21, Appl
18	685	60.0	130	1	US-08-570-923-21	Sequence 21, Appl
19	685	60.0	130	1	US-08-580-014-21	Sequence 21, Appl
20	685	60.0	130	4	US-09-079-785-21	Sequence 21, Appl
21	624	54.7	148	3	US-08-584-031-12	Sequence 12, Appl
22	388.5	34.0	125	1	US-08-225-989-20	Sequence 20, Appl
23	388.5	34.0	125	1	US-08-570-923-20	Sequence 20, Appl
24	388.5	34.0	125	1	US-08-580-014-20	Sequence 20, Appl
25	388.5	34.0	125	4	US-09-079-785-20	Sequence 20, Appl
26	229	20.1	52	4	US-09-369-494-17	Sequence 17, Appl
27	229	20.1	52	4	US-09-358-569D-15	Sequence 15, Appl

28	104	9.1	279	5	PCT-US95-00362-5	Sequence 5, Appl
29	88.5	7.8	309	1	US-08-236-918A-2	Sequence 2, Appl
30	85	7.4	291	1	US-08-670-354-6	Sequence 6, Appl
31	85	7.4	291	4	US-09-320-424-6	Sequence 6, Appl
32	85	7.4	291	5	PCT-US96-10895-6	Sequence 6, Appl
33	84	7.4	281	2	US-08-810-453-2	Sequence 2, Appl
34	84	7.4	281	3	US-08-815-190A-2	Sequence 2, Appl
35	84	7.4	281	4	US-09-290-640-25	Sequence 25, Appl
36	84	7.4	281	4	US-09-479-524-3	Sequence 3, Appl
37	84	7.4	281	5	PCT-US95-00362-2	Sequence 2, Appl
38	83.5	7.3	287	3	US-08-815-190A-16	Sequence 16, Appl
39	83	7.3	287	3	US-08-417-210A-140	Sequence 140, Appl
40	83	7.3	550	2	US-08-417-210A-137	Sequence 137, Appl
41	83	7.3	551	2	US-08-417-210A-143	Sequence 143, Appl
42	83	7.3	857	1	US-08-032-835-4	Sequence 4, Appl
43	83	7.3	857	1	US-08-388-809-4	Sequence 4, Appl
44	83	7.3	857	2	US-08-647-714-4	Sequence 4, Appl
45	82.5	7.2	183	4	US-09-105-343A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-225-989-19
; Sequence 19, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

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;
;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.3e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQVQGSVSPWRSTPWRSTSRYSFYLTALVCLVAVAIILVLVQKKDSTPNTTEK 60
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Db 61 APLKGGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
Qy 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLNSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
Db 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLNSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
Qy 181 LHYLVNSTISVRVDFNFQYVDNTFFPLDNVLSVFLYSSSD 220
Db 181 LHYLVNSTISVRVDFNFQYVDNTFFPLDNVLSVFLYSSSD 220

* RESULT 2
US-08-570-923-19
; Sequence 19, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
```

```
;
;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.3e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQVQGSVSPWRSTPWRSTSRYSFYLTALVCLVAVAIILVLVQKKDSTPNTTEK 60
Db 1 MQVQGSVSPWRSTPWRSTSRYSFYLTALVCLVAVAIILVLVQKKDSTPNTTEK 60
Qy 61 APLKGGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
Db 61 APLKGGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
Qy 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLNSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
Db 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLNSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
Qy 181 LHYLVNSTISVRVDFNFQYVDNTFFPLDNVLSVFLYSSSD 220
Db 181 LHYLVNSTISVRVDFNFQYVDNTFFPLDNVLSVFLYSSSD 220

RESULT 3
US-08-580-014-19
; Sequence 19, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:17:46 ; Search time 55.1 Seconds
(without alignments)
297.233 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYSNSD 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1118	100.0	234	2	CD30 ligand - huma
2	814.5	72.9	239	2	CD30 ligand - mouse
3	112	10.0	279	2	Fas ligand - mouse
4	96.5	8.6	234	1	tumor necrosis fac
5	94	8.4	235	2	tumor necrosis fac
6	93.5	8.4	547	2	rifampicin resista
7	90.5	8.1	281	2	Fas ligand - human
8	90	8.1	233	1	tumor necrosis fac
9	89	8.0	809	2	hypothetical prote
10	87.5	7.8	813	2	hypothetical prote
11	86	7.7	278	2	fes ligand - rat
12	85.5	7.6	309	2	4-1BB ligand - mou
13	85	7.6	235	1	tumor necrosis fac
14	84.5	7.6	232	1	tumor necrosis fac
15	83.5	7.5	234	1	tumor necrosis fac
16	83	7.4	636	2	hypothetical prote
17	83	7.4	1385	2	paraspinal crystal
18	82	7.3	513	2	hypothetical prote
19	82	7.3	1339	2	hypothetical prote
20	81.5	7.3	461	2	ID-myo-inositol-tr
21	81	7.2	233	1	tumor necrosis fac
22	81	7.2	547	2	hypothetical 61.6
23	81	7.2	1289	2	paraspinal crystal
24	80.5	7.2	430	2	ORF MSV157 hypothe
25	80.5	7.2	434	1	hypothetical prote
26	80.5	7.2	435	2	phosphoprotein pho
27	80	7.2	299	2	tumor necrosis fac
28	79.5	7.1	233	1	tumor necrosis fac
29	79	7.1	800	2	PET111 protein - y

RESULT 1
A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland, A.; Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <SMI>
A:Cross-references: GB:O09753; NID:g349277; PIDN:AAA74594.1; PID:g349278
C:Keywords: cytokine receptor; membrane protein; surface antigen

ALIGNMENTS

Query Match 100.0%; Score 1118; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHPAGSVASHLGTTSRSYFYLTATLALCLVETVATIMLVVQRTDIPNSPDNVPLKG 60
Db 20 MHPAGSVASHLGTTSRSYFYLTATLALCLVETVATIMLVVQRTDIPNSPDNVPLKG 79
QY 61 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIQPPGLY 120
Db 80 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIQPPGLY 139
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHIKQALVTVCESGMQTHVYONLSQFLDYIQ 180
Db 140 FIICQLQFLVQCPNNSVDLKLLELLINKHIKQALVTVCESGMQTHVYONLSQFLDYIQ 199
QY 181 VNTTISVNDVTFQVIDTSTFPLENVLISFLYSNSD 215
Db 200 VNTTISVNDVTFQVIDTSTFPLENVLISFLYSNSD 234

RESULT 2
B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland, A.; Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <SMI>
A:Cross-references: GB:U09754; NID:g349288; PIDN:AAA74595.1; PID:g349289
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 72.9%; Score 814.5; DB 2; Length 239;
Best Local Similarity 70.6%; Pred. No. 1.2e-69;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MHVPAGSVAS-----HLGTTTSRSEYVLTATLALCLVFTVATIMVLVQRTDIPNSPD 54
Db 20 MQVPGSVASPWRTSPWRTSRSEYVLTAL-VCLVAVAIILVLVQVRKDSPTTE 78
Qy 55 NVPLKGGNCSEDLCLIKRAPEKSWAYLOVAKHLNKTLSWNRKDGILHGVRYQDGNLVI 114
Db 79 KAPLKGNCSEDLCTLSKPSKSWAYLOVSKHLNKTLSWNRDGIHLIYQDGNLIV 138
Qy 115 QFGLYFIICQLQFLVQCPNNSVDLKLLELNKHKKQALVTVCEGQTKHVVYONLSQF 174
Db 139 QFGLYFIICQLQFLVQCSNHSVDLTQLLINSIKKQTLTVCEGVSQSNIVYONLSQF 198
Qy 175 LLDYLVQNTTISVNVDTFOYDTSFPLENVLSIFLYNSD 215
Db 199 LLHYLVQNTTISVRNDFQYVDTNTPFLDNVLSVFLYSSD 239

RESULT 3
A53062
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53062
R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A:Reference number: A53062; MUID:94185175
A:Accession: A53062
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TAK>
A:Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.0%; Score 112; DB 2; Length 279;
Best Local Similarity 22.6%; Pred. No. 0.0043;
Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;

Qy 33 FTVATIMVLVQRTDIPNSPDNVPPLKGGNCSEDLCLIKRAPEKSWAYLOVAKHLNKT 92
Db 115 FTNOSLAVSFEKQIANPSPSE-----KKEP--RSVAHLTGPHRSRI 156
Qy 93 KLSWKNK---DGILHGVRYQDGNLVIQPGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH 148
Db 157 PLEWEDRYGTALISGVYKKGGLVINETGLYFYVYKVFYRGQSCNQNPLNHKVVYMRNSKY 216
Qy 149 -----IKKQALVTVCEGSM-----QTKHVVYONLSQFL 176
Db 217 PEDLVLMEEKRLNYCTTGQIAHSSYLGAVFNLTSADHLVYVNIQSLSL 264

RESULT 4
JQ1344
tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JQ1344
R:Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A:Reference number: JQ1344; MUID:92084125

A:Accession: JQ1344
A:Molecule type: DNA
A:Residues: 1-234 <SUX>
A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:19-20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:146-178/disulfide bonds: #status predicted

Query Match 8.6%; Score 96.5; DB 1; Length 234;
Best Local Similarity 24.7%; Pred. No. 0.1; Mismatches 33; Indels 25; Gaps 8;
Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;

Qy 18 SYFVLTATLALCLVFTVATIMVLVQRTDIPNSPDNVPPLKGGNCSEDLCLIKRAPEK 77
Db 37 SFLLVAGATTFLCLLH---FGVIGPQREELPNAFQSI-----NPLAQTLRSSRTPSD 87
Qy 78 KSWAYLOVAKHLNKTLSW---NKDGIL-HGVRYQDGNLVIQPGLYFIICQLQFLVQ-C 132
Db 88 KPAHV-VANPOAEGOLWLSGRANALLANGVKLTQNLVPLDGLYLIYSQVLFKGGC 146
Qy 133 PNNSVDL--KLELLINKHIKQALVTVCEGSMQJ-----KHVYONLSQFLLDYLVQ 182
Db 147 PSTHVLTLTISRVAVSYPKYNLLSAIKSPCHTESPEQAEAKPWYEPIYLGCVFQLEK 206
Qy 183 TTISVNVDTFOYID 196
Db 207 DQLSAEINQPNYLD 220

RESULT 5
154490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: 154490
R:Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus
A:Reference number: 154490; MUID:92218012
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C:Genetics:
A:Gene: pTNF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19-20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.4%; Score 94; DB 2; Length 235;
Best Local Similarity 24.0%; Pred. No. 0.18; Mismatches 31; Indels 36; Gaps 8;
Matches 48; Conservative 31; Mismatches 85; Indels 36; Gaps 8;

Qy 18 SYFVLTATLALCLVFTVATIMVLVQRTDIPNSPDNVPPLKGGNCSEDLCLIKRAPEK 77
Db 37 SFLLVAGATTFLCLLH---NFGVIGPQREKEPN---NLPIGSMAQTTLRSSQNSSD 89
Qy 78 KSWAYLOVAKHLNKTLSWNRKDG-----ILHGVRYQDGNLVIQPGLYFIICQLQFLVQ-C 132
Db 90 KPAHV-VANHQVDQLEWLSRGANALLANGMDKQNLVLPADGLYLYVSQVLFKGGC 148

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2002, 08:31:35 ; Search time 33.56 Seconds
(without alignments)
234.891 Million cell updates/sec

Title: US-09-628-126-23

Perfect score: 1118

Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DTSTFPLENVLSIFLYNSND 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	234	1	TNF8_HUMAN
2	814.5	72.9	239	1	TNF8_MOUSE
3	112	10.0	279	1	FASL_MOUSE
4	96.5	8.6	234	1	TNFA_HORSE
5	94	8.4	233	1	TNFA_MACMU
6	94	8.4	235	1	TNFA_PERLE
7	92	8.2	233	1	TNFA_WACFA
8	90.5	8.1	281	1	FASL_HUMAN
9	90	8.1	233	1	TNFA_PAPHU
10	90	8.1	233	1	TNFA_PAPSP
11	89	8.0	809	1	YATA_SCHPO
12	86	7.7	278	1	FASL_RAT
13	85.5	7.6	309	1	41BL_MOUSE
14	85	7.6	233	1	TNFA_CANFA
15	85	7.6	235	1	TNFA_MOUSE
16	85	7.6	1220	1	C5AC_BACTU
17	84.5	7.6	232	1	TNFA_PIG
18	83.5	7.5	234	1	TNFA_SHEEP
19	83	7.4	1385	1	C5AA_BACUD
20	81.5	7.3	461	1	IP3K_HUMAN
21	81	7.2	233	1	TNFA_HUMAN
22	81	7.2	233	1	TNFA_WARMO
23	81	7.2	541	1	YHFX_ECOLI
24	81	7.2	1289	1	C5AB_BACUD
25	80.5	7.2	499	1	PPP5_RAT
26	80	7.2	229	1	TNFA_CEREL
27	80	7.2	235	1	TNFA_RAT
28	79.5	7.1	233	1	TNFA_BOVIN
29	79	7.1	800	1	PT11_YEAST
30	78.5	7.0	234	1	TNFA_CAVPO
31	78.5	7.0	426	1	MMML_YEAST
32	77.5	6.9	670	1	DD18_HUMAN
33	76	6.8	479	1	PAP1_VACCC

34	76	6.8	829	1	TOP1_XENLA
35	76	6.8	982	1	MSHM_SARGL
36	75.5	6.8	807	1	SUS1_ARATH
37	75	6.7	427	1	SYS_BUCAP
38	75	6.7	499	1	PPP5_HUMAN
39	74.5	6.7	745	1	RNR_BUCAI
40	74	6.6	541	1	YHXB_ECO57
41	74	6.6	851	1	NUD1_YEAST
42	74	6.6	2136	1	YCF2_MARPO
43	73.5	6.6	1178	1	PH81_YEAST
44	73	6.5	606	1	LEPA_BORBU
45	72.5	6.5	1900	1	STT4_YEAST

ALIGNMENTS

RESULT	1
TNF8_HUMAN	
ID	TNF8_HUMAN
AC	P32971; STANDARD; PRT; 234 AA.
DT	01-OCT-1993 (Rel. 27, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN	TNFSF8 OR CD30LG OR CD30L.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=93313964; PubMed=8391931;
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA	Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA	Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT	ligand defines an emerging family of cytokines with homology to
RT	TNF."
RL	Cell 73:1349-1360(1993).
CC	-!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC	T CELLS.
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC	-!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry; htm".
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd153.htm".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: L09753; AAA74594.1; -
DR	PIR: A40710; A40710.
DR	MIM: 603875; -
DR	InterPro: IPR003638; TNF_8.
DR	InterPro: IPR000478; TNF_family.
DR	Pfam: PF00229; TNF; 1.
DR	ProDom: PD033087; TNF_8; 1.
DR	SMART: SM00207; TNF; 1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PSS0049; TNF_2; 1.
DR	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT	DOMAIN 1 37
FT	TRANSNEM 38 62
FT	DOMAIN 63 234
FT	CARBOHYD 81
FT	CARBOHYD 109 109
FT	CARBOHYD 153 153

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FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 100.0%; Score 1118; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPNVPLKG 60
    |||||
DB 20 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPNVPLKG 79
    |||||

QY 61 GNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRYODGNLVIOFPGLY 120
    |||||
DB 80 GNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRYODGNLVIOFPGLY 139
    |||||

QY 121 FIICQLOFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQLLDYLO 180
    |||||
DB 140 FIICQLOFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQLLDYLO 199
    |||||

QY 181 VNTTISVNDVTFQYIDTSTFPLENLSIFLYSNSD 215
    |||||
DB 200 VNTTISVNDVTFQYIDTSTFPLENLSIFLYSNSD 234
    |||||

RESULT 2
TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=F-cell;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RA "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; L09754; AAA74595.1;
DR PIR; B40710; B40710.
DR MGD; MGI:86328; Tnfsf8.
DR InterPro; IPR0003638; TNF8.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD023087; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
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DR PROSITE; PS0049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 43 CYTOPLASMIC ANCHOR (POTENTIAL).
FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 72.9%; Score 814.5; DB 1; Length 239;
Best Local Similarity 70.6%; Pred. No. 2.5e-69;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTTSSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSD 54
    |||||
DB 20 MQVQPGSVASPMWRSTRPMWRSTRSYFYLSTTAL-VCLVAVAILVLVQKDSPTNTTE 78
    |||||

QY 55 NVPLKGGNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRYODGNLVI 114
    |||||
DB 79 KAPLKGNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRYODGNLVI 138
    |||||

QY 115 QPGLYFTICQLOFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQL 174
    |||||
DB 139 QPGLYFTICQLOFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQL 198
    |||||

QY 175 LLDYLQVNTTISVNDVTFQYIDTSTFPLENLSIFLYSNSD 215
    |||||
DB 199 LLHVLQVNSTISVRVDFQYVDTNFTPLDNLVSLVFLYSSSD 239
    |||||

RESULT 3
FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; O61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLIG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand."
RL Cell 76:969-976(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family."
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster."
RL Immunity 1:131-136(1994).
RN [4]
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ult No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1094	97.9		234	4	O43404	O43404 homo sapien
2	100	8.9		169	11	O9W90	O9wr90 marmota mon
3	96.5	8.6		215	6	Q9BEB8	Q9beeb erlinaeus e
4	95.5	8.5		280	6	Q9BDN1	Q9bdn1 cercocebus
5	94.5	8.5		234	6	Q9TTJ3	Q9ttj3 equus cabal
6	93.5	8.4		547	12	Q98269	Q98269 molluscus c
7	93	8.3		217	11	Q9ERG6	Q9erg6 peromyscus
8	92	8.2		280	6	Q9MYL6	Q9myl6 macaca neme
9	92	8.2		280	6	Q9BDN5	Q9bdn5 macaca mulla
10	83.5	8.0		896	10	Q9M9B0	Q9mb0 arabidopsis
11	88.5	7.9	217	6	Q9BEG1	Q9beg1 bradypus tr	
12	88	7.9	1109	5	Q9YH7	Q9ygh7 caenorhabdi	
13	87.5	7.8	216	6	Q9BEC4	Q9bec4 talpa europ	
14	87.5	7.8	813	4	Q9Y4N0	Q9y4n0 homo sapien	
15	87.5	7.8	1003	4	Q9P207	Q9p207 homo sapien	
16	85.5	7.6	462	2	Q9CM44	Q9cm44 pasteurella	
17	85	7.6	282	6	Q9BEA8	Q9bea8 sus scrofa	
18	85	7.6	761	3	Q9UVJ1	Q9uvj1 candida alb	
19	84.5	7.6	232	4	Q9UIV3	Q9uiv3 homo sapien	

Qv 67 GN

67 GNCSEDI.C.T.I.K.KRAPEKKSWAYI.OVAKH.I.NKTKI.SWNKDG.TI.HGVRYODGNI.VIO

|||||
Db 80 GNCSEDLCLIKRAPFKSWAYLQVAKHLNKTLSWKNKDLGRLGRVYQDGNLVIOFFGLY 139
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMQKHYQNLSQFLDLYLQ 180
Db 140 FIICQLQFLVQCPNNSVDLKLXELLINKHKIKKQALVTVCESGMQKHYQNLSQFLDLYLQ 199
QY 181 VNTTISVNDTFFQYIDTSTPLENVLNLSIFLYNSD 215
Db 200 VNTTISVNDTFFQYIDTSTPLENVLNLSIFLYNSD 234
RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL; AF152368; AAD38387.1;
DR InterPro; IPR000478; TNE family.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
FT NON_TER 1 169
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 8.9%; Score 100; DB 11; Length 169;
Best Local Similarity 24.6%; Pred. No. 0.025;
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;
QY 71 LKRAPFKSWAYLQVAKHLNKTLSWKNK---GILHGVRYQDGNLVIOFFGLYFIICQLQ 127
Db 40 LKRA-----AHLTKRPNSSRSPLEWEDTYGISLSGVKYQKGLVINDTGLYFVYSKIY 93
QY 128 FLVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTKH 166
Db 94 FRGQSCNNPPLSHKVVYKNSKYPQDLVLMGKMMNYCTTGQMWARSYLGAVENFTSNDH 153
QY 167 VYONLSQFL 176
Db 154 LYVNSLSL 163

RESULT 3
Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (FRAGMENT).
GN TNFA.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1;
FT NON_TER 1 215
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 8.6%; Score 96.5; DB 6; Length 215;
Best Local Similarity 23.3%; Pred. No. 0.075;
Matches 47; Conservative 36; Mismatches 76; Indels 43; Gaps 10;
QY 18 SYFYLTATLALCLVFTVATIMVLVQRTDPSIPNDVPLKGGNCSEDLCLLK--RAP 75
Db 28 SFFLVAGATTFLCLLH---FGVIGPQRDE---FPDNIQLNNA-----LAQTLRSSRTQ 74
QY 76 FKSWAYLQVAKHLNKTLSWKNKDG---ILHGVRYQDGNLVIOFFGLYFIICQLQFLVQ 131
Db 75 SDKPVAHV-VASIKSEGQLMESEVANALLANGMLTDNQLVPLDGLYLYISQVLFKQ 133
QY 132 -CPNNSVDLKLLELLINKHK-----QALVTVCES-----GMOTKHYQNLSQF 174
Db 134 GCPSTHV-----FLTHNIKRYAVSYQKDVNLLSAIKSPCQSETPEGAERWYEFYILG 187
QY 175 LLDYLQVNTTISVNDTFFQYID 196
Db 188 GVFOLEKGDRLSAEINLPDILD 209

RESULT 4
Q9BDN1 PRELIMINARY; PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE CD95L PROTEIN.
GN CD95L.
OS Cercoebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercoebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF34847; AAK37606.1;
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 8.5%; Score 95.5; DB 6; Length 280;
Best Local Similarity 27.1%; Pred. No. 0.13;
Matches 35; Conservative 21; Mismatches 46; Indels 27; Gaps 6;
QY 75 PFKKSW---AYLQVAKHLNKTLSWKNK-GI--LHGVRYQDGNLVIOFFGLYFIICQLQ 128
Db 137 PEKKEQRKVAHLTKGPNRSRSPLEWEDTYGISLSGVKYKGLVINETGLYFVYSKVYF 196
QY 129 LVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTKH 167
Db 197 RGQSTNLPLSHKYYMRNRSKYPODLVMMGKMMSYCTTGQMWAHSSYLGAVENLTSTDL 256
QY 168 YONLSQFL 176